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OM protein - protein search, using sw model

Run on: July 26, 2004, 11:12:29 ; Search time 8.924 Seconds
(without alignments)
728.215 Million cell updates/sec

Title: US-09-719-533A-3_COPY_298_320
Perfect score: 138
Sequence: 1 CTTPAQGTSMFPSCCTKPTDRN 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_25Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	228	2 AAR67368	Mutant He
2	138	100.0	228	2 AAR67369	Mutant He
3	138	100.0	228	2 AAR67370	Mutant He
4	138	100.0	400	3 AAY44349	Human hep
5	134	97.1	56	2 AAW34087	Mutant HB
6	131	94.9	71	2 AAW65506	Hepatitis
7	131	94.9	71	3 AAY85119	Hepatitis
8	131	94.9	400	4 AAG66929	HBV genot
9	127	92.0	36	2 AAW65474	Hepatitis
10	127	92.0	56	2 AAW34084	HBV surfa
11	126	91.3	24	2 AAR50965	Peptide c
12	126	91.3	24	2 AAR50961	Amino aci
13	126	91.3	24	2 AAR50968	Peptide c
14	126	91.3	24	2 AAR50964	Peptide c
15	126	91.3	24	2 AAR84433	HBV surfa
16	126	91.3	24	2 AAY04027	HBSAg pep
17	126	91.3	24	2 AAE25520	Hepatitis
18	126	91.3	71	2 AAW65505	Hepatitis
19	126	91.3	71	3 AAY85118	Hepatitis
20	126	91.3	209	2 AAR55288	Deduced s
21	126	91.3	226	2 AAR33252	HBSAg enc
22	126	91.3	226	2 AAR55282	Deduced s
23	126	91.3	226	5 AAW52894	Hepatitis
24	126	91.3	250	2 AAR11496	RP142/HBS
25	126	91.3	251	2 AAR11495	RP135/HBS

26	126	91.3	280	2 AAR10850	Modified
27	126	91.3	281	2 AAR55281	Deduced s
28	126	91.3	281	4 AAE02620	HBSAg pre
29	126	91.3	281	5 AAW52693	Hepatitis
30	126	91.3	387	2 AAR10852	Modified
31	126	91.3	388	2 AAR10851	Modified
32	126	91.3	389	2 AAR55287	Deduced s
33	126	91.3	389	5 AAW52682	Hepatitis
34	126	91.3	390	4 AAE02621	Chimeric
35	126	91.3	400	4 AAG66928	HBV genot
36	126	91.3	424	2 AAR37797	RTS* prote
37	126	91.3	424	2 AAR37796	RTS* prote
38	126	91.3	531	4 AAE02622	Chimeric
39	126	90.6	56	2 AAW34088	Mutant HB
40	124	89.9	49	5 AAG68210	HBV wild
41	124	89.9	49	5 AAG68211	HBV Leban
42	124	89.9	61	6 ABF55074	Hepatitis
43	124	89.9	71	2 AAW65508	Hepatitis
44	124	89.9	226	2 AAW62826	Hepatitis
45	124	89.9	226	4 AAG62930	Amino aci

ALIGNMENTS

RESULT 1
AAR67368
ID AAR67368 standard; protein; 228 AA.
XX AAR67368;
AC

XX
DT 25-MAR-2003 (revised)
DT 22-SEP-1995 (first entry)
XX
DE Mutant Hepatitis B virus surface antigen sequence.
XX
KW Hepatitis B virus; HBV; mutant; detection; surface antigen; HBSAg;
KW detection; vaccine; diagnostic; prognosis; therapy.
XX
OS Hepatitis B virus.
XX
FH Key Location/Qualifiers
FT Region 123..124
FT /note= "Dipeptide encoded by insertion sequence."
XX
FN WO9426904-A1.
XX
PD 24-NOV-1994.
XX
PF 09-MAY-1994; 94WO-US005090.
XX
PR 07-MAY-1993; 93US-00059031.
XX
PA (ABBO) ABBOTT LAB.
XX (UNIU) UNIV GLASGOW.
XX
PI Carman W, Decker RH, Wallace L, Mimms LT, Solomon LR;
XX
XX WPI; 1995-006799/01.
XX N-PSDB; AAQ75318.
XX
PT New mutant hepatitis B virus polynucleotide - used to develop prods. for
PT diagnosis, prognosis, therapy and studies involving hepatitis B
PT infection.
XX
XX Example 2; Page 49-50; 59pp; English.
XX
CC The mutant hepatitis B virus (HBV) polypeptide comprises an insertion of
CC two amino acid residues at position 122 of the HBV surface antigen
CC (HBSAg). The polynucleotide encoding the mutant polypeptide can be used
CC for detection of mutant HBV and for the production of the polypeptide
CC which can be used in vaccines for the treatment of infection. Antibodies
CC against such polypeptides can be used for detecting the mutant HBV

CC antigen. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 228 AA;

Query Match 100.0%; Score 138; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTAAGTSMFPSCCCTKPTDRN 23
Db 126 CTTAAGTSMFPSCCCTKPTDRN 148

RESULT 2

AAR67369
ID AAR67369 standard; protein; 228 AA.

XX AAR67369;

XX 25-MAR-2003 (revised)
DT 22-SEP-1995 (first entry)

DE Mutant Hepatitis B virus surface antigen sequence.

XX Hepatitis B virus; HBV; mutant; detection; surface antigen; HBsAg;
KW detection; vaccine; diagnostic; prognosis; therapy.

OS Hepatitis B virus.

PH Key Location/Qualifiers
FT Region 123..124
/note= "Dipeptide encoded by insertion sequence."

XX WO9426904-A1.
XX 24-NOV-1994.

XX 09-MAY-1994; 94WO-US005090.
XX 07-MAY-1993; 93US-00059031.

XX (ABBO) ABBOTT LAB.
PA (UNIU) UNIV GLASGOW.

XX Carman W, Decker RH, Wallace L, Mimms LT, Solomon LR;
XX WPI; 1995-006799/01.
XX New mutant hepatitis B virus polynucleotide - used to develop prods. for
PT diagnosis, prognosis, therapy and studies involving hepatitis B
PT infection.

XX Example 2; Page 50-51; 59pp; English.

PS The mutant hepatitis B virus (HBV) polypeptide comprises an insertion of
XX two amino acid residues at position 122 of the HBV surface antigen
CC (HBsAg). The polynucleotide encoding the mutant polypeptide can be used
CC for detection of mutant HBV and for the production of the polypeptide
CC which can be used in vaccines for the treatment of infection. Antibodies
CC against such polypeptides can be used for detecting the mutant HBV
CC antigen. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 228 AA;

Query Match 100.0%; Score 138; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTAAGTSMFPSCCCTKPTDRN 23
Db 126 CTTAAGTSMFPSCCCTKPTDRN 148

RESULT 3

AAR67370
ID AAR67370 standard; protein; 228 AA.

XX AAR67370;

XX 25-MAR-2003 (revised)
DT 22-SEP-1995 (first entry)

XX Mutant Hepatitis B virus surface antigen sequence.

XX Hepatitis B virus; HBV; mutant; detection; surface antigen; HBsAg;
KW detection; vaccine; diagnostic; prognosis; therapy.

OS Hepatitis B virus.

XX Key Location/Qualifiers
FT Region 123..124
/note= "Dipeptide encoded by insertion sequence."

XX WO9426904-A1.
XX 24-NOV-1994.

XX 09-MAY-1994; 94WO-US005090.
XX 07-MAY-1993; 93US-00059031.

XX (ABBO) ABBOTT LAB.
PA (UNIU) UNIV GLASGOW.
XX Carman W, Decker RH, Wallace L, Mimms LT, Solomon LR;
XX WPI; 1995-006799/01.

XX New mutant hepatitis B virus polynucleotide - used to develop prods. for
PT diagnosis, prognosis, therapy and studies involving hepatitis B
PT infection.
XX Example 2; Page 51-52; 59pp; English.

XX The mutant hepatitis B virus (HBV) polypeptide comprises an insertion of
CC two amino acid residues at position 122 of the HBV surface antigen
CC (HBsAg). The polynucleotide encoding the mutant polypeptide can be used
CC for detection of mutant HBV and for the production of the polypeptide
CC which can be used in vaccines for the treatment of infection. Antibodies
CC against such polypeptides can be used for detecting the mutant HBV
CC antigen. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 228 AA;

Query Match 100.0%; Score 138; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTAAGTSMFPSCCCTKPTDRN 23
Db 126 CTTAAGTSMFPSCCCTKPTDRN 148

RESULT 4

AAY44349
ID AAY44349 standard; protein; 400 AA.

XX AAY44349;

XX 06-AUG-2003 (revised)
DT 14-MAR-2000 (first entry)

XX Human hepatitis B virus large surface antigen.

XX HBIG; Hepatitis B immunoglobulin; HBV; Hepatitis B virus;
KW large surface antigen; mutant major surface antigen; HBV infection;

KW human hepatitis B virus; hepatocellular carcinoma;
 KW human hepatitis B virus surface antigen- 'S'- 145 Singapore strain.
 XX
 OS Hepatitis B virus.
 PH Key Location/Qualifiers
 FT Misc-difference 123..400
 FT /note= "No corresponding nucleotides in SEQ ID NO.1"
 XX
 PN WO9966047-A1.
 XX
 XX 23-DEC-1999.
 XX
 XX 19-JUN-1998; 98WO-SG000045.
 XX
 XX 19-JUN-1998; 98WO-SG000045.
 XX
 PA (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.
 XX
 XX Oon CJ, Lim GK, Leong AL, Zhao Y, Chen WN;
 PI WPI; 2000-106103/09.
 DR N-PSDB; AA229453.
 DR
 XX New vaccine-escape mutant of hepatitis B virus and related proteins,
 PT nucleic acids and antibodies, useful for diagnosis, prevention and
 PT treatment.
 PT
 XX Claim 9; Fig 5; 65pp; English.
 XX
 CC The present sequence is the large surface antigen deduced from the mutant
 CC human hepatitis B viral genome. This was isolated from a male, 11 year
 CC old Singaporean child which had received standard HBIG and HB vaccine and
 CC was infected with the mutated strain designated human hepatitis B virus
 CC surface antigen- 'S'- 145 Singapore strain a year later. This protein can
 CC be produced by recombinant technology and used in developing polyclonal
 CC or monoclonal antibodies and as a source of diagnostic oligonucleotides.
 CC The mutated major surface antigen is used to raise specific antibodies,
 CC to identify specific binding agents and, in vaccines or compositions for
 CC treatment or prevention of HBV infection and hepatocellular carcinoma.
 CC Antibodies are used in diagnosis or for screening donated body fluids or
 CC tissues. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 400 AA;
 Query Match 100.0%; Score 138; DB 3; Length 400;
 Best Local Similarity 100.0%; Pred. No. 5.6e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
 DB 298 CTTPAQGTSMFPSCCCTKPTDRN 320
 RESULT 5
 AA34087
 ID AAW34087 standard; peptide; 56 AA.
 XX
 AC AAW34087;
 DT 27-APR-1998 (first entry)
 XX
 DE Mutant HBV surface antigen fragment.
 XX
 KW HBV; hepatitis b virus; surface antigen; HBSAg; monoclonal antibody;
 KW immunisation; HBV infection; vaccine; blood screening; muten.
 XX
 OS Hepatitis B virus.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 37
 FT /note= "Gly to Arg mutation"
 XX

PN WO9740164-A1.
 XX
 PD 30-OCT-1997.
 XX
 XX 25-APR-1997; 97WO-GB001161.
 XX
 XX 25-APR-1996; 96GB-00008626.
 XX
 XX (MURE-) MUREX DIAGNOSTICS CORP.
 XX
 XX Tedder R, Ijaz S, Ferns RB;
 PI WPI; 1997-535848/49.
 DR
 XX Monoclonal antibodies to hepatitis B virus surface antigen, HBSAg - used
 PT to develop products for the detection, treatment and prevention of
 PT hepatitis B virus infection.
 XX
 XX Claim 10; Page; 64pp; English.
 XX
 CC This sequence represents a fragment of a mutant of the hepatitis b virus
 CC (HBV) surface antigen (HBSAg), designated HBSAg I (SZ HBSAg). This
 CC sequence was isolated from patients with naturally occurring variants of
 CC the wild type HBSAg fragment shown in AAW34084. This sequence is
 CC recognised by the antibody of the invention. The antibody of the
 CC invention is a monoclonal antibody (MAb) is capable of binding
 CC specifically to HBSAg and to at least two mutant forms of HBSAg. The MAb
 CC can bind to both wild type and mutant forms of HBV. They can be used
 CC therapeutically or prophylactically for passive immunisation against HBV
 CC infection or to define an epitope for use as a vaccine in active
 CC immunisation. They can also be used for detecting HBSAg, for diagnosis of
 CC HBV infections and for blood screening
 XX
 SQ Sequence 56 AA;
 Query Match 97.1%; Score 134; DB 2; Length 56;
 Best Local Similarity 95.7%; Pred. No. 2.7e-10;
 Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
 DB 16 CTTPAQGTSMFPSCCCTKPTDRN 38
 RESULT 6
 AAW65506
 ID AAW65506 standard; peptide; 71 AA.
 XX
 XX AAW65506;
 AC
 DT 27-AUG-2003 (revised)
 DT 12-OCT-1998 (first entry)
 XX
 DE Hepatitis B surface antigen peptide fragment (geno B).
 XX
 KW Annexin V; hepatitis B surface antigen; immunogen; vaccine;
 KW hepatitis delta virus; infection; HBSAg.
 XX
 OS Hepatitis B virus.
 XX
 XX WO9829442-A1.
 XX
 PD 09-JUL-1998.
 XX
 XX 23-DEC-1997; 97WO-EP007268.
 XX
 XX 30-DEC-1996; 96EP-00870164.
 XX
 XX 11-JUL-1997; 97EP-00870103.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA
 XX Depla B, Maertens G, Yap S, De Meyer S;
 PI
 XX

DR WPI; 1998-388040/33.
 XX Immunogenic polypeptide from hepatitis B surface antigen - useful in,
 PT e.g. vaccine against hepatitis B virus or hepatitis delta virus
 PT infection.
 XX
 XX Disclosure; Page 35; 71pp; English.
 XX
 XX The invention relates to an immunogenic peptide derived from hepatitis B
 CC surface antigen (HBsAg) which competes with the hepatitis B surface
 CC antigen/annexin V interaction or which binds a compound or antibody
 CC competing with the hepatitis B surface antigen/annexin V interaction.
 CC Also claimed are: (1) a combination of the immunogenic peptide and a
 CC negatively charged phospholipid; (2) a peptide composition comprising the
 CC immunogenic peptide; (3) a vaccine comprising the immunogenic peptide as
 CC an active substance; (4) antibodies which specifically bind to the
 CC peptide and inhibit binding of HBsAg to annexin V, and (5) a therapeutic
 CC composition comprising as an active substance the antibodies of (4). The
 CC vaccine of (3), and the therapeutic composition of (5), can be used as an
 CC inoculum to vaccinate humans against an infection with hepatitis B
 CC and/or hepatitis delta virus. The immunogenic peptide can be used in a
 CC method to detect antibodies which are capable of competing with the
 CC hepatitis B and/or hepatitis delta virus surface antigen/annexin V
 CC interaction. The immunogenic peptide can also be used to screen for drugs
 CC which block the binding between annexin V and the peptide, and as a
 CC therapeutic to treat humans infected with hepatitis B virus and/or
 CC hepatitis delta virus. The present sequence is shown in the
 CC specification. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 XX Sequence 71 AA;
 SQ
 Query Match 94.9%; Score 131; DB 2; Length 71;
 Best Local Similarity 95.7%; Pred. No. 8.5e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
 DB 26 CTTPAQGTSMFPSCCCTKPTDGN 48
 RESULT 7
 ID AAY85119 standard; peptide; 71 AA.
 AC AAY85119;
 XX
 DT 06-AUG-2003 (revised)
 DT 20-JUN-2000 (first entry)
 XX
 DE Hepatitis B virus surface antigen B amino acid sequence.
 KW Annexin binding epitope; hepatitis B virus; hepatitis D virus; influenza;
 KW benzodiazepine; binding inhibitor; cytomegalovirus; viral infection;
 KW benzodiazepine.
 OS Hepatitis B virus.
 XX WO200012547-A2.
 PN
 PD 09-MAR-2000.
 XX
 PF 25-AUG-1999; 99WO-EP006231.
 XX
 PR 01-SEP-1998; 98EP-00870196.
 PR 29-MAR-1999; 99EP-00870062.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Depla E, Moereels H, Maertens G;
 XX
 DR WPI; 2000-256586/22.
 XX
 PT New benzodiazepine and benzothiazepine derivatives, useful for treating

PT or preventing viral infection, contain peptides that include an annexin-
 PT binding epitope.
 XX Example 5; Page 29; 60pp; English.
 XX
 XX This sequence represents a fragment of the hepatitis B virus surface
 CC antigen B amino acid sequence. The antigen sequence is used to determine
 CC the best sequence to use as a source of peptides for the composition of
 CC the invention. The invention relates to benzodiazepine derivatives
 CC derivatised with at least one peptide containing an annexin binding
 CC epitope of an annexin binding protein (see AAY85082-Y85115) or its
 CC fragment. Annexins are calcium dependent phospholipid binding proteins.
 CC 1,4-benzodiazepines and 1,4-benzothiazepines can bind to annexin V, as
 CC can the hepatitis B small surface antigen. The compositions of the
 CC invention bind to cell surface annexins, and inhibit the binding and
 CC entry of viruses to the cell. The benzodiazepine derivatives and some
 CC related known compounds, are used to treat or prevent diseases involving
 CC protein interactions with annexins, particularly viral infections and
 CC specifically hepatitis B and/or D, cytomegalovirus or influenza or to
 CC screen for compounds that block binding between annexins and their
 CC interacting proteins. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 XX Sequence 71 AA;
 SQ
 Query Match 94.9%; Score 131; DB 3; Length 71;
 Best Local Similarity 95.7%; Pred. No. 8.5e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
 DB 26 CTTPAQGTSMFPSCCCTKPTDGN 48
 RESULT 8
 ID AAG66929 standard; protein; 400 AA.
 XX
 AC AAG66929;
 XX
 DT 19-OCT-2001 (first entry)
 DT
 DE HBV genotype B pres1/pres2/HBsAg polypeptide.
 XX
 KW Hepatitis B virus; HBV; preCore; Core; pres1; pres2; HBS; HBx; HBPol;
 KW HBsAg; antiviral; vaccine; genotype G; genotyping; HBcAg; HBeAg.
 OS Hepatitis B virus.
 XX WO200140279-A2.
 PN
 PD 07-JUN-2001.
 XX
 PF 20-NOV-2000; 2000WO-BP011526.
 XX
 PR 03-DEC-1999; 99EP-00870252.
 PR 07-DEC-1999; 99US-0169287P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Stuyver L, Van Geyt C, De Gendt S;
 XX
 DR WPI; 2001-374785/39.
 XX
 PT Novel isolated and/or purified hepatitis B virus polypeptide and
 PT polynucleotide sequences that are phylogenetically different from HBV
 PT Genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
 PT therapy.
 XX
 XX Example 3; Fig 6; 94pp; English.
 XX
 XX The invention relates to the complete nucleic acid sequence of a new
 CC human hepatitis B virus (HBV) genotype, provisionally named genotype G.
 CC This genotype was found with a high prevalence in patients chronically

CC infected with HBV and residing in Europe and the USA. The invention
 CC relates to a fully defined sequence of 3248 nucleotides as given in
 CC specification, a sequence with 92% identity to the given sequence, or
 CC sequence that is degenerate to the mentioned sequences. These
 CC polynucleotides are useful for HBV genotyping. The proteins encoded by
 CC the polynucleotides are useful for detecting antibodies in a biological
 CC sample. Ligands that bind to the proteins and antibodies directed against
 CC the proteins are useful for detecting the proteins and for detecting
 CC HBsAg and HBeAg (precursor proteins). They are also useful for
 CC preparing a vaccine or medicament for treating HBV infections. The
 CC present sequence is provided in an amino acid sequence alignment of the
 CC pres1, pres2 and HBeAg open reading frame of the different HBV genotypes
 XX
 SQ Sequence 400 AA;

Query Match 94.9%; Score 131; DB 4; Length 400;
 Best Local Similarity 95.7%; Pred. No. 4.6e-09;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
 DB 298 CTTPAQGTSMFPSCCCTKPTDGN 320

RESULT 9
 AAW65474
 ID AAW65474 standard; peptide; 36 AA.

XX AAW65474;
 XX
 XX 27-AUG-2003 (revised)
 DT 12-OCT-1998 (first entry)
 XX
 XX Hepatitis B surface antigen derived peptide (IGP 80).
 XX
 XX Annexin V; hepatitis B surface antigen; immunogen; vaccine;
 KW hepatitis delta virus; infection; HBeAg.

XX Synthetic.
 OS Hepatitis B virus.

XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminally biotinylated"
 FT

XX WO9829442-A1.

XX 09-JUL-1998.

XX 23-DEC-1997; 97WO-EP007268.

XX 30-DEC-1996; 96EP-00870164.

XX 11-JUL-1997; 97EP-00870103.

XX (INNO-) INNOGENETICS NV.

XX Depla E, Maertens G, Yap S, De Meyer S;

XX WPI; 1998-388040/33.

XX Immunogenic polypeptide from hepatitis B surface antigen - useful in,
 PT e.g. vaccine against hepatitis B virus or hepatitis delta virus
 PT infection.

XX Example 3; Page 35; 71pp; English.

XX The invention relates to an immunogenic peptide derived from hepatitis B
 CC surface antigen (HBsAg) which competes with the hepatitis B surface
 CC antigen/annexin V interaction or which binds a compound or antibody
 CC competing with the hepatitis B surface antigen/annexin V interaction.
 CC Also claimed are: (1) a combination of the immunogenic peptide and a
 CC negatively charged phospholipid; (2) a peptide composition comprising the
 CC immunogenic peptide; (3) a vaccine comprising the immunogenic peptide as

CC an active substance; (4) antibodies which specifically bind to the
 CC peptide and inhibit binding of HBeAg to annexin V, and (5) a therapeutic
 CC composition comprising as an active substance the antibodies of (4). The
 CC vaccine of (3), and the therapeutic composition of (5), can be used as an
 CC inoculum to vaccinate humans against an infection with hepatitis B
 CC and/or hepatitis delta virus. The immunogenic peptide can be used in a
 CC method to detect antibodies which are capable of competing with the
 CC hepatitis B and/or hepatitis Delta virus surface antigen/annexin V
 CC interaction. The immunogenic peptide can also be used to screen for drugs
 CC which block the binding between annexin V and the peptide, and as a
 CC therapeutic to treat humans infected with hepatitis B virus and/or
 CC hepatitis Delta virus. The present sequence represents one of the peptide
 CC fragments derived from HBsAg which were synthesised to map the annexin V-
 CC binding site on HBsAg. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 36 AA;

Query Match 92.0%; Score 127; DB 2; Length 36;

Best Local Similarity 91.3%; Pred. No. 1.5e-09;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
 DB 3 CTTPAQGTSMFPSCCCTKPTDSN 25

RESULT 10
 AAW34084
 ID AAW34084 standard; peptide; 56 AA.

XX AAW34084;

XX 27-APR-1998 (first entry)

XX HBV surface antigen fragment.

XX HBV; hepatitis B virus; surface antigen; HBeAg; monoclonal antibody;
 KW immunisation; HBV infection; vaccine; blood screening.

XX Hepatitis B virus.

XX WO9740164-A1.

XX 30-OCT-1997.

XX 25-APR-1997; 97WO-GB001161.

XX 25-APR-1996; 96GB-00008626.

XX (MURE-) MUREX DIAGNOSTICS CORP.

XX Tedder R, Ijaz S, Ferns RB;

XX WPI; 1997-535848/49.

XX N-PSDB; AAT93040.

XX Monoclonal antibodies to hepatitis B virus surface antigen, HBsAg - used
 PT to develop products for the detection, treatment and prevention of
 PT hepatitis B virus infection.

XX Disclosure; Fig 1b; 64pp; English.

XX This sequence represents a fragment of the hepatitis B virus (HBV)
 CC surface antigen (HBsAg). This sequence is recognised by the antibody of
 CC the invention. The antibody of the invention is a monoclonal antibody
 CC (MAB) is capable of binding specifically to HBsAg and to at least two
 CC mutant forms of HBsAg. The MABs can bind to both wild type and mutant
 CC forms of HBV. They can be used therapeutically or prophylactically for
 CC passive immunisation against HBV infection or to define an epitope for
 CC use as a vaccine in active immunisation. They can also be used for
 CC detecting HBsAg, for diagnosis of HBV infections and for blood screening

XX Sequence 56 AA;

```

Query Match          92.0%; Score 127; DB 2; Length 56;
Best Local Similarity 91.3%; Pred. No. 2.3e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
    |||||
DQ 16 CTTPAQGTSMFPSCCCTKPTSDGN 38
    |||||

RESULT 11
AAR50965
ID AAR50965 standard; peptide; 24 AA.
XX
AC AAR50965;
XX
DT 25-MAR-2003 (revised)
DT 14-OCT-1994 (first entry)
XX
DE Peptide cross reactive with anti-HBsAg antiserum.
XX
KW Hepatitis B virus; HBV; epitope; antigen; HBsAg; diagnosis; detection;
KW vaccine; treatment; antiserum; adv; surface antigen; viral infection.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 10
FT /label= Other.
FT /note= "Met (O)."
XX
FN WO9405698-A1.
XX
PD 17-MAR-1994.
XX
PF 30-AUG-1993; 93WO-EP002342.
XX
PR 01-SEP-1992; 92AT-00001746.
XX
PA (UNNA-) UNITED NATIONS IND DEV ORG.
XX
PI Manivel V, Rao KV, Panda SK;
XX
DR WPI; 1994-101123/12.
XX
PT Peptide(s) for use in diagnosis or vaccines for hepatitis B virus -
PT comprising oligomers of an epitope sequence of hepatitis B surface
PT antigen.
XX
PS Claim 2; Page 14; 26pp; English.
XX
CC The peptide shows cross reactivity with anti-hepatitis B surface antigen
CC (HBsAg) antiserum. The peptide comprises the "a" epitope of HBsAg, a
CC group specific determinant of HBsAg. It can be used for the diagnosis of
CC hepatitis B virus infection and in vaccines against the virus.
CC particularly in combination with alum as adjuvant and with a myristic
CC acid residue added to the amino terminus of the peptide. This sequence is
CC an analogue of the sequence described in AAR50961. See also in AAR50962-
CC 70. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 24 AA;

Query Match          91.3%; Score 126; DB 2; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.3e-09;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
    |||||
DQ 1 CTTPAQGTSMFPSCCCTKPTDGN 23
    |||||

RESULT 13
AAR50968
ID AAR50968 standard; peptide; 24 AA.
XX
AC AAR50968;
XX
DT 25-MAR-2003 (revised)
DT 14-OCT-1994 (first entry)
XX
DE Peptide cross reactive with anti-HBsAg antiserum.
XX
KW Hepatitis B virus; HBV; epitope; antigen; HBsAg; diagnosis; detection;
KW vaccine; treatment; antiserum; adv; surface antigen; viral infection.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 18
FT /label= Melys.

```

XX PN WO9405698-A1.
 XX PD 17-MAR-1994.
 XX PF 30-AUG-1993; 93WO-EP002342.
 XX PR 01-SEP-1992; 92AT-00001746.
 XX PA (UNNA-) UNITED NATIONS IND DEV ORG.
 XX PI Manivel V, Rao KV, Panda SK;
 XX DR WPI; 1994-101123/12.
 XX PT Peptide(s) for use in diagnosis or vaccines for hepatitis B virus -
 PT comprising oligomers of an epitope sequence of hepatitis B surface
 PT antigen.
 XX PS Claim 2; Page 14; 26pp; English.
 XX CC The peptide shows cross reactivity with anti-hepatitis B surface antigen
 CC (HBsAg) antiserum. The peptide comprises the "a" epitope of HBsAg, a
 CC group specific determinant of HBsAg. It can be used for the diagnosis of
 CC hepatitis B virus infection and in vaccines against the virus.
 CC particularly in combination with alum as adjuvant and with a myristic
 CC acid residue added to the amino terminus of the peptide. This sequence is
 CC an analogue of the sequence described in AAR50961. See also in AAR50962-
 CC 70. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 24 AA;
 Query Match 91.3%; Score 126; DB 2; Length 24;
 Best Local Similarity 91.3%; Pred. No. 1.3e-09;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 DB 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 RESULT 14
 AAR50964
 ID AAR50964 standard; peptide; 24 AA.
 AC AAR50964;
 XX DT 25-MAR-2003 (revised)
 XX DT 14-OCT-1994 (first entry)
 XX DE Peptide cross reactive with anti-HBsAg antiserum.
 XX KW Hepatitis B virus; HBV; epitope; antigen; HBsAg; diagnosis; detection;
 XX KW vaccine; treatment; antiserum; adv; surface antigen; viral infection.
 XX OS Synthetic.
 XX PN WO9405698-A1.
 XX PD 17-MAR-1994.
 XX PF 30-AUG-1993; 93WO-EP002342.
 XX PR 01-SEP-1992; 92AT-00001746.
 XX PA (UNNA-) UNITED NATIONS IND DEV ORG.
 XX PI Manivel V, Rao KV, Panda SK;
 XX DR WPI; 1994-101123/12.
 XX PT Peptide(s) for use in diagnosis or vaccines for hepatitis B virus -
 PT comprising oligomers of an epitope sequence of hepatitis B surface

PT antigen.
 XX PS Claim 2; Page 14; 26pp; English.
 XX CC The peptide shows cross reactivity with anti-hepatitis B surface antigen
 CC (HBsAg) antiserum. The peptide comprises the "a" epitope of HBsAg, a
 CC group specific determinant of HBsAg. It can be used for the diagnosis of
 CC hepatitis B virus infection and in vaccines against the virus,
 CC particularly in combination with alum as adjuvant and with a myristic
 CC acid residue added to the amino terminus of the peptide. This sequence is
 CC an analogue of the sequence described in AAR50961. See also in AAR50962-
 CC 70. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 24 AA;
 Query Match 91.3%; Score 126; DB 2; Length 24;
 Best Local Similarity 91.3%; Pred. No. 1.3e-09;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 DB 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 RESULT 15
 AAR94433
 ID AAR94433 standard; peptide; 24 AA.
 XX AC AAR94433;
 XX DT 27-AUG-2003 (revised)
 XX DT 31-MAY-1996 (first entry)
 XX DE HBV surface protein B-cell epitope.
 XX KW Molecular presentation; PHV; virion-like particle; capsid protein;
 XX KW capsomer; RNA-2 gene; epitope; HBV; vaccine.
 XX OS Hepatitis B virus.
 XX PN WO9605293-A1.
 XX PD 22-FEB-1996.
 XX PF 04-AUG-1995; 95WO-EP003114.
 XX PR 08-AUG-1994; 94AT-00001545.
 XX PA (UNNA-) UNITED NATIONS IND DEV ORG.
 XX PI Baralle FE, Scodeller E, Tisminetzky S;
 XX DR WPI; 1996-139691/14.
 XX PT New molecular presentation system - comprising a viral protein from a
 PT small insect virus in which heterologous amino acid sequences are
 PT inserted.
 XX PS Disclosure; Page 7; 39pp; English.
 XX CC The B-cell epitope (AAR94433) of the hepatitis B virus surface protein
 CC may be inserted into the outward-directed L1, L2, L3, L2 or L3 loop of
 CC the Flock House virus capsid protein (AAR8755). The capsid protein
 CC provides a conformationally suitable location for this (or other, see
 CC AAR9430-32 and AAR94434-45) heterologous peptides. A molecular
 CC presentation system is obtd. The FHV recombinant capsomer can be
 CC expressed in E. coli. Alternatively, expression in insect cells using a
 CC baculovirus vector results in prodn. of mature virus-like particles.
 CC (Updated on 27-AUG-2003 to correct OS field.)
 XX SQ Sequence 24 AA;
 Query Match 91.3%; Score 126; DB 2; Length 24;

Best Local Similarity 91.3%; Pred. No. 1.3e-09;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
| | | | | | | | | | | | | | | | | | | | |
Db 1 CTTPAQGTSMFPSCCCTKPTDGN 23

Search completed: July 26, 2004, 11:27:12
Job time : 9.924 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2004, 11:25:30 ; Search time 2.668 seconds
(without alignments)
445.051 Million cell updates/sec

Title: US-09-719-533A-3_COPY_298_320
Perfect score: 138
Sequence: 1 CTPAQGTSMFPSCCCTKPTDRN 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	228	1	US-08-447-591-2
2	138	100.0	228	1	US-08-447-591-3
3	138	100.0	228	1	US-08-447-591-4
4	138	100.0	228	1	US-08-450-943-2
5	138	100.0	228	1	US-08-450-943-3
6	138	100.0	228	1	US-08-450-943-4
7	138	100.0	228	1	US-08-059-031-2
8	138	100.0	228	1	US-08-059-031-3
9	138	100.0	228	1	US-08-059-031-4
10	138	100.0	228	2	US-08-450-942-2
11	138	100.0	228	2	US-08-450-942-3
12	138	100.0	228	2	US-08-450-942-4
13	138	100.0	228	5	PCT-US94-05090-2
14	138	100.0	228	5	PCT-US94-05090-3
15	138	100.0	228	5	PCT-US94-05090-4
16	131	94.9	154	3	US-09-193-104-13
17	131	94.9	154	3	US-09-193-104-14
18	131	94.9	154	3	US-09-193-104-15
19	131	94.9	154	3	US-09-193-104-16
20	131	94.9	154	3	US-09-193-104-17
21	126	91.3	24	2	US-08-776-585-6
22	126	91.3	24	4	US-09-282-826-3
23	126	91.3	154	3	US-09-193-104-20
24	126	91.3	225	6	5436139-4
25	126	91.3	226	6	5196194-21
26	126	91.3	226	6	5436139-5
27	126	91.3	395	6	5196194-18

US-08-447-591-2

Sequence 2, Application US/08447591

Patent No. 5591440

GENERAL INFORMATION:

APPLICANT: CARMAN, WILLIAM

APPLICANT: DECKER, RICHARD H

APPLICANT: WALLACE, LESLEY

APPLICANT: MIMMS, LARRY T

APPLICANT: SOLOMON, LARRY R

TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

STREET: ONE ABBOTT PARK ROAD

CITY: ABBOTT PARK

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/447,591

FILING DATE: 23-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 08/059,031

APPLICATION NUMBER: US 08/059,031

FILING DATE: 07-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: POREMSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5347.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 228 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-447-591-2

Query Match 100.0%; Score 138; DB 1; Length 228;

Best Local Similarity 100.0%; Pred. No. 2.7e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 2

US-08-447-591-3
; Sequence 3, Application US/08447591
; Patent No. 5591440
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: ONE ABBOTT PARK ROAD D377/AP6D
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,591
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,031
; FILING DATE: 07-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-447-591-3

Query Match 100.0%; Score 138; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 2,7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 3

US-08-447-591-4
; Sequence 4, Application US/08447591
; Patent No. 5591440
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: ONE ABBOTT PARK ROAD D377/AP6D
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,591
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,031
; FILING DATE: 07-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-447-591-4

Query Match 100.0%; Score 138; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 2,7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 4

US-08-450-943-2
; Sequence 2, Application US/08450943
; Patent No. 5593825
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLIS, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: ONE ABBOTT PARK ROAD D377/AP6D
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,943
; FILING DATE:

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; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-943-2

Query Match 100.0%; Score 138; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 5
US-08-450-943-3
; Sequence 3, Application US/08450943
; Patent No. 5593825
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLIS, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,943
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-943-3

Query Match 100.0%; Score 138; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 6
US-08-450-943-4
; Sequence 4, Application US/08450943
; Patent No. 5593825
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLIS, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,943
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-943-4

Query Match 100.0%; Score 138; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 7
US-08-059-031-2
; Sequence 2, Application US/08059031
; Patent No. 5595739
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 6
US-08-450-943-4
; Sequence 4, Application US/08450943
; Patent No. 5593825
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLIS, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,943
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-943-4

Query Match 100.0%; Score 138; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 7
US-08-059-031-2
; Sequence 2, Application US/08059031
; Patent No. 5595739
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
;; STREET: ONE ABBOTT PARK ROAD
;; CITY: ABBOTT PARK
;; STATE: IL USA
;; COUNTRY: USA
;; ZIP: 60064-3500
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/059,031
;; FILING DATE:
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FOREMSKI, PRISCILLA E.
;; REGISTRATION NUMBER: 33,207
;; REFERENCE/DOCKET NUMBER: 5347.US.01
;; TELEPHONE: 708-937-6365
;; TELEFAX: 708-938-2623
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 228 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-059-031-2

Query Match 100.0%; Score 138; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 8
US-08-059-031-3
; Sequence 3, Application US/08059031
; Patent No. 5595739
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MINMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/059,031
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 708-937-6365
;; TELEFAX: 708-938-2623
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 228 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-059-031-3

Query Match 100.0%; Score 138; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 9
US-08-059-031-4
; Sequence 4, Application US/08059031
; Patent No. 5595739
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MINMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/059,031
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-059-031-4

Query Match 100.0%; Score 138; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148


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RESULT 10
US-08-450-942-2
; Sequence 2, Application US/08450942
; Patent No. 5925512
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,942
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-942-2
;
; Query Match 100.0%; Score 138; DB 2; Length 228;
; Best Local Similarity 100.0%; Pred. No. 2.7e-11;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 11
US-08-450-942-3
; Sequence 3, Application US/08450942
; Patent No. 5925512
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,942
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-942-2
;
; Query Match 100.0%; Score 138; DB 2; Length 228;
; Best Local Similarity 100.0%; Pred. No. 2.7e-11;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 12
US-08-450-942-4
; Sequence 4, Application US/08450942
; Patent No. 5925512
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,942
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,942
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-942-3
;
; Query Match 100.0%; Score 138; DB 2; Length 228;
; Best Local Similarity 100.0%; Pred. No. 2.7e-11;
; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 12
US-08-450-942-4
; Sequence 4, Application US/08450942
; Patent No. 5925512
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,942
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-942-4

Query Match 100.0%; Score 138; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 13

PCT-US94-05090-2

; Sequence 2, Application PC/TUS9405090

; GENERAL INFORMATION:

; APPLICANT: CARMAN, WILLIAM

; APPLICANT: DECKER, RICHARD H

; APPLICANT: WALLACE, LESLEY

; APPLICANT: MIMMS, LARRY T

; APPLICANT: SOLOMON, LARRY R

; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

; STREET: ONE ABBOTT PARK ROAD

; CITY: ABBOTT PARK

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION NUMBER: PCT/US94/05090

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: FOREMSKI, PRISCILLA E.

; REGISTRATION NUMBER: 33,207

; REFERENCE/DOCKET NUMBER: 5347.US.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-6365

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 228 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US94-05090-2

Query Match 100.0%; Score 138; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 14

PCT-US94-05090-3

; Sequence 3, Application PC/TUS9405090

; GENERAL INFORMATION:

; APPLICANT: CARMAN, WILLIAM

; APPLICANT: DECKER, RICHARD H

; APPLICANT: WALLACE, LESLEY

Mon Jul 26 11:38:46 2004

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; NAME: POREBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-05090-4

Query Match      100.0%; Score 138; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTPAQGTSMFPSCCCTKPTDRN 23
      |||||
Db     126 CTTPAQGTSMFPSCCCTKPTDRN 148
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Search completed: July 26, 2004, 11:30:10
Job time : 2.668 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model
Run on: July 26, 2004, 11:29:00 ; Search time 7.544 Seconds
(without alignments)
954.738 Million cell updates/sec

Title: US-09-719-533a-3_COPY_298_320
Perfect score: 138
Sequence: 1 CTTPAQGTSMFPSCCCKPTDRN 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1288442 seqs, 313154207 residues

Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubaa/US09D_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	91.3	678	15	US-10-365-620-29
2	126	91.3	678	15	US-10-365-620-32
3	125	90.6	400	14	US-10-224-999A-3461
4	124	89.9	49	10	US-09-823-077B-5
5	124	89.9	49	10	US-09-823-077B-6
6	124	89.9	61	9	US-09-821-877-5
7	124	89.9	226	14	US-10-169-668-5
8	124	89.9	229	9	US-09-821-877-8
9	124	89.9	389	9	US-09-821-877-2
10	124	89.9	389	14	US-10-169-668-6
11	124	89.1	157	14	US-10-260-451-20
12	122	88.4	38	12	US-10-312-045-34
13	122	88.4	48	12	US-10-312-045-36
14	121	87.7	226	16	US-10-335-774-2
15	121	87.7	226	16	US-10-335-774-40

ALIGNMENTS

US-10-365-620-29

Sequence 29, Application US/10365620

Publication No. US20040001853A1

GENERAL INFORMATION:

APPLICANT: George, Rajan

APPLICANT: Tyrell, Lorne

APPLICANT: No. US20040001853A1aim, Antoine

TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response

FILE REFERENCE: 656.0016

CURRENT APPLICATION NUMBER: US/10/365,620

CURRENT FILING DATE: 2003-02-13

PRIOR APPLICATION NUMBER: US60/423,578

PRIOR FILING DATE: 2003-11-05

PRIOR APPLICATION NUMBER: 60/390,564

PRIOR FILING DATE: 2002-06-20

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn version 3.2

SEQ ID NO 29

LENGTH: 678

TYPE: PRT

ORGANISM: Hepatitis B virus

US-10-365-620-29

Query Match 91.3%; Score 126; DB 15; Length 678;

Best Local Similarity 91.3%; Pred. No. 5.8e+08;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTTPAQGTSMFPSCCCKPTDRN 23

Db 326 CTTPAQGTSMFPSCCCKPTDRN 348

RESULT 2

US-10-365-620-32

Sequence 32, Application US/10365620

Publication No. US20040001853A1

GENERAL INFORMATION:

Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||||:|||||:|
Db 25 CTTPAQGTSMFPSCCCTKPSDGN 47

RESULT 7
US-10-169-668-5
; Sequence 5, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
; APPLICANT: BIOMERIEUX
; APPLICANT: INSEERM
; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
; TITLE OF INVENTION: CONSTITUENTS AND USES THEREOF
; FILE REFERENCE: IFB 99 INS HBVM
; CURRENT APPLICATION NUMBER: US/10/169,668
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 226
; TYPE: PRT
; ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-5

Query Match 89.9%; Score 124; DB 14; Length 226;
Best Local Similarity 87.0%; Pred. No. 3.8e-08;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||||:|||||:|
Db 124 CTTPAQGTSMFPSCCCTKPSDGN 146

RESULT 8
US-09-821-877-8
; Sequence 8, Application US/09821877
; Patent No. US20020177124A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Coleman, Paul F.
; APPLICANT: Mushahwar, Isa K.
; TITLE OF INVENTION: Hepatitis B Virus Surface Antigen Mutant
; TITLE OF INVENTION: And Methods Of Detection Thereof
; FILE REFERENCE: 6794.US.01
; CURRENT APPLICATION NUMBER: US/09/821,877
; CURRENT FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Hepatitis B Virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (126)... (126)
; OTHER INFORMATION: Xaa = A or T at position 126
; NAME/KEY: VARIANT
; LOCATION: (202)... (202)
; OTHER INFORMATION: Xaa = L or W at position 202
; NAME/KEY: VARIANT
; LOCATION: (210)... (210)
; OTHER INFORMATION: Xaa = T or S at position 210
US-09-821-877-8

Query Match 89.9%; Score 124; DB 9; Length 229;
Best Local Similarity 87.0%; Pred. No. 3.8e-08;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||||:|||||:|

Db 127 CTTPAQGTSMFPSCCCTKPSDGN 149

RESULT 9
US-09-821-877-2
; Sequence 2, Application US/09821877
; Patent No. US20020177124A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Coleman, Paul F.
; APPLICANT: Mushahwar, Isa K.
; TITLE OF INVENTION: Hepatitis B Virus Surface Antigen Mutant
; TITLE OF INVENTION: And Methods Of Detection Thereof
; FILE REFERENCE: 6794.US.01
; CURRENT APPLICATION NUMBER: US/09/821,877
; CURRENT FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Hepatitis B Virus
US-09-821-877-2

Query Match 89.9%; Score 124; DB 9; Length 389;
Best Local Similarity 87.0%; Pred. No. 6.3e-08;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||||:|||||:|
Db 287 CTTPAQGTSMFPSCCCTKPSDGN 309

RESULT 10
US-10-169-668-6
; Sequence 6, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
; APPLICANT: BIOMERIEUX
; APPLICANT: INSEERM
; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
; FILE REFERENCE: IFB 99 INS HBVM
; CURRENT APPLICATION NUMBER: US/10/169,668
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 389
; TYPE: PRT
; ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-6

Query Match 89.9%; Score 124; DB 14; Length 389;
Best Local Similarity 87.0%; Pred. No. 6.3e-08;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||||:|||||:|
Db 287 CTTPAQGTSMFPSCCCTKPSDGN 309

RESULT 11
US-10-260-451-20
; Sequence 20, Application US/10260451
; Publication No. US20030124096A1
; GENERAL INFORMATION:
; APPLICANT: LOCARNINI, STEPHEN A
; APPLICANT: BARHOLOMEUSZ, ANGELINE I
; APPLICANT: AYE, THEIN T
; APPLICANT: DEMAN, ROBERT A
; TITLE OF INVENTION: VIRAL VARIANTS AND METHODS FOR DETECTING SAME
; FILE REFERENCE: 2551-28

APPLICANT: JING-LI LI
 APPLICANT: PAUL RIMBES
 TITLE OF INVENTION: Expression of Immunogenic Hepatitis B Surface Antigens In


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; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 09/471,573
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Plant optimized HBsAg amino acid sequence
; NAME/KEY: misc_feature
; OTHER INFORMATION: Plant optimized HBsAg amino acid sequence
US-10-335-774-40

Query Match      87.7%; Score 121; DB 16; Length 226;
Best Local Similarity 87.0%; Pred No: 9.1e-05;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1  CTTPAQGTSMFPSCCCTKPTDRN 23
Db      124 CTTPAQGTSMFPSCCCTKPSDGN 146

Search completed: July 26, 2004, 11:38:30
Job time : 7.544 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2004, 11:23:20 ; Search time 2.116 Seconds
(without alignments)
1045.560 Million cell updates/sec

Title: US-09-719-533A-3_COPY_298_320
Perfect score: 138
Sequence: 1 CTTPAQGTSMFPSCCCTKPTDRN 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.78.*

2: PIR1.*

3: PIR2.*

4: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	131	94.9	226	1 JQ1570	major surface anti
2	131	94.9	226	2 JQ2058	surface antigen -
3	131	94.9	226	2 JQ2057	surface antigen -
4	131	94.9	226	2 JQ2061	surface antigen -
5	131	94.9	226	2 JQ2060	surface antigen -
6	131	94.9	226	2 JQ2062	surface antigen -
7	131	94.9	389	1 SAVLJ2	large surface anti
8	131	94.9	389	1 SAVLJ3	large surface anti
9	127	92.0	226	1 SAVLAD	major surface anti
10	127	92.0	226	1 JQ1574	major surface anti
11	127	92.0	226	2 JQ2101	surface antigen -
12	126	91.3	226	1 SAVLHV	major surface anti
13	126	91.3	226	1 JQ1577	major surface anti
14	126	91.3	226	2 JQ2045	surface antigen -
15	126	91.3	226	2 JQ2052	surface antigen -
16	126	91.3	226	2 JQ2046	surface antigen -
17	126	91.3	226	2 JQ2055	surface antigen -
18	126	91.3	226	2 JQ2050	surface antigen -
19	126	91.3	226	2 JQ2053	surface antigen -
20	126	91.3	226	2 JQ2048	surface antigen -
21	126	91.3	400	1 SAVLVD	large surface anti
22	126	91.3	400	1 SAVLKS	large surface anti
23	126	91.3	400	1 JQ1575	major surface anti
24	125	90.6	389	1 SAVLJ1	major surface anti
25	124	89.9	226	1 JQ1571	major surface anti
26	124	89.9	226	2 JQ2081	surface antigen -
27	124	89.9	226	2 JQ2083	surface antigen -
28	124	89.9	226	2 JQ2079	surface antigen -
29	124	89.9	226	2 JQ2075	surface antigen -

ALIGNMENTS

RESULT 1

JQ1570

major surface antigen - hepatitis B virus (subtype ayw1, strain Pl)

C;Species: hepatitis B virus, HBV

A;Note: host Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999

C;Accession: JQ1570

R;Order, H.; Hammes, B.; Loeffdahl, S.; Courouce, A.M.; Magnius, L.O.

J. Gen. Virol. 73, 1201-1208, 1992

A;Title: Comparison of the amino acid sequences of nine different serotypes of hepatitis B virus

A;Reference number: JQ1570; PMID:92268879; PMID:1588323

A;Accession: JQ1570

A;Molecule type: DNA

A;Residues: 1-226 <NOR>

A;Cross-references: GB:X75660; NID:G416078; PIDN:CAA53347.1; PID:G416079

C;Genetics:

A;Gene: S

C;Superfamily: hepatitis B virus surface antigen

C;Keywords: surface antigen

Query Match 94.9%; Score 131; DB 1; Length 226;
Best Local Similarity 95.7%; Pred. NO. 3.2e-10;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23

DB 124 CTTPAQGTSMFPSCCCTKPTDGN 146

RESULT 2

JQ2058

surface antigen - hepatitis B virus (subtype adw2, strain 1764/92)

C;Species: hepatitis B virus, HBV

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C;Accession: JQ2058

R;Order, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius

J. Gen. Virol. 74, 1341-1348, 1993

A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin

A;Reference number: JQ2044; PMID:93329382; PMID:8336122

A;Contents: Genogroup B

A;Accession: JQ2058

A;Molecule type: DNA

A;Residues: 1-226 <NOR>

C;Genetics:

A;Gene: S

C;Superfamily: hepatitis B virus surface antigen

C;Keywords: surface antigen

Query Match 94.9%; Score 131; DB 2; Length 226;
Best Local Similarity 95.7%; Pred. NO. 3.2e-10;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 Db 124 CTTPAQGTSMFPSCCCTKPTDGN 146

RESULT 3

Query Match 94.9%; Score 131; DB 2; Length 226;
 Best Local Similarity 95.7%; Pred. No. 3.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 C:Superfamily: hepatitis B virus (subtype adw2, strain Sru)
 C:Species: hepatitis B virus, HBV
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: JQ2057
 R:Order, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus,
 J. Gen. Virol. 74, 1341-1348, 1993
 A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
 A:Reference number: JQ2044; MUID:93329382; PMID:8336122
 A:Contents: Genogroup B
 A:Accession: JQ2057
 A:Molecule type: DNA
 A:Residues: 1-226 <NOR>
 C:Genetics:
 A:Gene: S
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen

Query Match 94.9%; Score 131; DB 2; Length 226;
 Best Local Similarity 95.7%; Pred. No. 3.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 Db 124 CTTPAQGTSMFPSCCCTKPTDGN 146

RESULT 4

Query Match 94.9%; Score 131; DB 2; Length 226;
 Best Local Similarity 95.7%; Pred. No. 3.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 C:Superfamily: hepatitis B virus (subtype ayw1, strain Ngu)
 C:Species: hepatitis B virus, HBV
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: JQ2061
 R:Order, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus,
 J. Gen. Virol. 74, 1341-1348, 1993
 A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
 A:Reference number: JQ2044; MUID:93329382; PMID:8336122
 A:Contents: Genogroup B
 A:Accession: JQ2061
 A:Molecule type: DNA
 A:Residues: 1-226 <NOR>
 C:Genetics:
 A:Gene: S
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen

Query Match 94.9%; Score 131; DB 2; Length 226;
 Best Local Similarity 95.7%; Pred. No. 3.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 Db 124 CTTPAQGTSMFPSCCCTKPTDGN 146

RESULT 5

Query Match 94.9%; Score 131; DB 2; Length 226;
 Best Local Similarity 95.7%; Pred. No. 3.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 C:Superfamily: hepatitis B virus (subtype ayw1, strain Pon)
 C:Species: hepatitis B virus, HBV
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: JQ2060
 R:Order, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus,
 J. Gen. Virol. 74, 1341-1348, 1993
 A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
 A:Reference number: JQ2044; MUID:93329382; PMID:8336122
 A:Contents: Genogroup B
 A:Accession: JQ2060

A:Molecule type: DNA
 A:Residues: 1-226 <NOR>
 C:Genetics:

A:Gene: S
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen

Query Match 94.9%; Score 131; DB 2; Length 226;
 Best Local Similarity 95.7%; Pred. No. 3.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 Db 124 CTTPAQGTSMFPSCCCTKPTDGN 146

RESULT 6

Query Match 94.9%; Score 131; DB 2; Length 226;
 Best Local Similarity 95.7%; Pred. No. 3.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 C:Superfamily: hepatitis B virus (subtype ayw1, strains Vut and Meu)
 C:Species: hepatitis B virus, HBV
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: JQ2062; PQ0580
 R:Order, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus,
 J. Gen. Virol. 74, 1341-1348, 1993
 A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
 A:Reference number: JQ2044; MUID:93329382; PMID:8336122
 A:Contents: Genogroup B
 A:Accession: JQ2062
 A:Molecule type: DNA
 A:Residues: 1-226 <NOR>
 C:Genetics:
 A:Gene: S
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen

Query Match 94.9%; Score 131; DB 2; Length 226;
 Best Local Similarity 95.7%; Pred. No. 3.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 Db 124 CTTPAQGTSMFPSCCCTKPTDGN 146

RESULT 7

Query Match 94.9%; Score 131; DB 2; Length 226;
 Best Local Similarity 95.7%; Pred. No. 3.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 C:Superfamily: hepatitis B virus (subtype adw, strain Okinawa/PODW282)
 C:Species: hepatitis B virus, HBV
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 14-Nov-1997
 C:Accession: H28925
 R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosoewignjo, R.I.; Imai, M.; Miyakawa, Y.; M
 J. Gen. Virol. 69, 2575-2583, 1988
 A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surf
 A:Reference number: JS0253; MUID:89010694; PMID:3171552
 A:Accession: H28925
 A:Molecule type: DNA
 A:Residues: 1-389 <OKA>
 A:Cross-references: GB:D00330; NID:G221498
 C:Genetics:
 A:Gene: pre-S1/pre-S2/S
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: glycoprotein; surface antigen
 F:109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>

Query Match 94.9%; Score 131; DB 2; Length 226;
 Best Local Similarity 95.7%; Pred. No. 3.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 Db 124 CTTPAQGTSMFPSCCCTKPTDGN 146

RESULT 7

Query Match 94.9%; Score 131; DB 2; Length 226;
 Best Local Similarity 95.7%; Pred. No. 3.2e-10;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 C:Superfamily: hepatitis B virus (subtype adw, strain Okinawa/PODW282)
 C:Species: hepatitis B virus, HBV
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 14-Nov-1997
 C:Accession: H28925
 R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosoewignjo, R.I.; Imai, M.; Miyakawa, Y.; M
 J. Gen. Virol. 69, 2575-2583, 1988
 A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surf
 A:Reference number: JS0253; MUID:89010694; PMID:3171552
 A:Accession: H28925
 A:Molecule type: DNA
 A:Residues: 1-389 <OKA>
 A:Cross-references: GB:D00330; NID:G221498
 C:Genetics:
 A:Gene: pre-S1/pre-S2/S
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: glycoprotein; surface antigen
 F:109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>

F:164-389/Product: major surface antigen (gene S) #status predicted <MSA>
F:4,112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.9%; Score 131; DB 1; Length 389;
Best Local Similarity 95.7%; Pred. No. 4.9e-10;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||||
DB 287 CTTPAQGTSMFPSCCCTKPTDRN 309
|||||

RESULT 8
SAVLJ3
large surface antigen - hepatitis B virus (subtype adw, strain Indonesia/p1DW420)
N:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 07-May-1999
C:Accession: J28925; PQ0570
R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosuewignjo, R.I.; Imai, M.; Miyakawa, Y.; M
J. Gen. Virol. 69, 2575-2583, 1988
A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of surf
A:Reference number: JS0283; MUID:89010694; PMID:3171552
A:Accession: J28925
A:Molecule type: DNA
A:Residues: 1-389 <OKA>
A:Cross-references: GB:D00331; NID:g221499
A:Experimental source: subtype adw, strain Indonesia/p1DW420
R:Norder, H.; Courouce, A.M.; Magnius, L.O.
J. Gen. Virol. 73, 3141-3145, 1992
A:Title: Molecular basis of hepatitis B virus serotype variations within the four major
A:Reference number: PQ0453; MUID:93107848; PMID:1469353
A:Accession: PQ0570
A:Molecule type: DNA
A:Residues: 264-343 <NOR>
A:Experimental source: subtype adw2, Sru
C:Genetics:
A:Gene: pre-S1/pre-S2/S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
F:109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F:164-389/Product: major surface antigen (gene S) #status predicted <MSA>
F:4,112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.9%; Score 131; DB 1; Length 389;
Best Local Similarity 95.7%; Pred. No. 4.9e-10;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||||
DB 287 CTTPAQGTSMFPSCCCTKPTDRN 309
|||||

RESULT 9
SAVLAD
major surface antigen - hepatitis B virus (subtype ad)
C:Species: hepatitis B virus, HBV
A:Note: host Homo sapiens (man)
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
C:Accession: PL0053
R:Okamoto, H.; Omi, S.; Wang, Y.; Itoh, Y.; Tsuda, F.; Tanaka, T.; Akahane, Y.; Miyakawa
Mol. Immunol. 26, 197-205, 1989
A:Title: The loss of subtypic determinants in alleles, d/y or w/r, on hepatitis B surfac
A:Reference number: PL0053; MUID:89143494; PMID:2465492
A:Accession: PL0053
A:Molecule type: DNA
A:Residues: 1-226 <OKA>
A:Cross-references: GB:M27765; NID:g329706; PIDN:AAA45518.1; PID:g329707
C:Genetics:
A:Gene: S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
F:3/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.0%; Score 127; DB 1; Length 226;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||||
DB 124 CTTPAQGTSMFPSCCCTKPSDGN 146
|||||

RESULT 10
JQ1574
major surface antigen - hepatitis B virus (subtype ayr, strain P5)
C:Species: hepatitis B virus, HBV
A:Note: host Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
C:Accession: JQ1574
R:Norder, H.; Hammes, B.; Loeffdahl, S.; Courouce, A.M.; Magnius, L.O.
J. Gen. Virol. 73, 1201-1208, 1992
A:Title: Comparison of the amino acid sequences of nine different serotypes of hepatiti
A:Reference number: JQ1570; MUID:92268879; PMID:1588323
A:Accession: JQ1574
A:Molecule type: DNA
A:Residues: 1-226 <NOR>
A:Cross-references: GB:X75667; NID:g416080; PIDN:CAA53363.1; PID:g416081
C:Genetics:
A:Gene: S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
F:3/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.0%; Score 127; DB 1; Length 226;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||||
DB 124 CTTPAQGTSMFPSCCCTKPSDGN 146
|||||

RESULT 11
JQ2101
surface antigen - hepatitis B virus (subtype ayr, strain PVC)
C:Species: hepatitis B virus, HBV
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: JQ2101; PQ0609
R:Norder, H.; Hammes, B.; Lee, S.D.; Bille, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius
J. Gen. Virol. 74, 1341-1348, 1993
A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origi
A:Reference number: JQ2044; MUID:93329382; PMID:8336122
A:Contents: genogroup C
A:Accession: JQ2101
A:Molecule type: DNA
A:Residues: 1-226 <NOR>
R:Norder, H.; Courouce, A.M.; Magnius, L.O.
J. Gen. Virol. 73, 3141-3145, 1992
A:Title: Molecular basis of hepatitis B virus serotype variations within the four major
A:Reference number: PQ0453; MUID:93107848; PMID:1469353
A:Accession: PQ0609
A:Molecule type: DNA
A:Residues: 101-180 <NO2>
C:Genetics:
A:Gene: S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: surface antigen

Query Match 92.0%; Score 127; DB 2; Length 226;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||||
DB 124 CTTPAQGTSMFPSCCCTKPSDGN 146
|||||

RESULT 12

SAVLHV

major surface antigen - hepatitis B virus

C:Species: hepatitis B virus, HBV

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999

C:Accession: J02093

R:Rivkina, M.B.; Lunin, V.G.; Mahov, A.M.; Tikchonenko, T.I.; Kukain, R.A.

Gene 64, 285-296, 1988

A:Title: Nucleotide sequence of integrated hepatitis B virus DNA and human flanking region

A:Reference number: J02093; MUID:86297159; PMID:2841200

A:Accession: J02093

A:Molecule type: DNA

A:Residues: 1-226 <RIV>

A:Cross-references: GB:M21030; MID:9329702; PIDN:AAA45516.1; PID:G329703

C:Genetics:

A:Gene: S

C:Superfamily: hepatitis B virus surface antigen

C:Keywords: glycoprotein; surface antigen

F:3/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.3%; Score 126; DB 1; Length 226;

Best Local Similarity 91.3%; Pred. No. 1.5e-09;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTAAGTSMFPSCCCTKPTDGN 23

Db 124 CTTAAGNSMFPSCCCTKPTDGN 146

RESULT 13

JQ1577

major surface antigen - hepatitis B virus (subtype ayw1)

C:Species: hepatitis B virus, HBV

A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999

C:Accession: JQ1577; JQ2049; PQ0573

R:Norder, H.; Hammes, B.; Loefldahl, S.; Courouce, A.M.; Magnus, L.O.

J. Gen. Virol. 73, 1201-1208, 1992

A:Title: Comparison of the amino acid sequences of nine different serotypes of hepatitis B virus

A:Reference number: JQ1570; MUID:92266879; PMID:1586323

A:Accession: JQ1577

A:Molecule type: DNA

A:Residues: 1-226 <NOR>

A:Cross-references: GB:X75669; MID:G416076; PIDN:CAA53365.1; PID:G416077

A:Experimental source: subtype ayw1, strain CNTS-5

R:Norder, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus,

J. Gen. Virol. 74, 1341-1348, 1993

A:Title: Genetic relatedness of hepatitis B virus strains of diverse geographical origin

A:Reference number: JQ2044; MUID:93329382; PMID:8336122

A:Contents: Genogroup A

A:Accession: JQ2049

A:Molecule type: DNA

A:Residues: 1-226 <NOR>

A:Experimental source: subtype ayw1, strain Mam

R:Norder, H.; Courouce, A.M.; Magnus, L.O.

J. Gen. Virol. 73, 3141-3145, 1992

A:Title: Molecular basis of hepatitis B virus serotype variations within the four major

A:Reference number: PQ0453; MUID:93107846; PMID:1469353

A:Accession: PQ0573

A:Molecule type: DNA

A:Residues: 101-180 <NOR>

A:Experimental source: subtype ayw1, strain Mam

C:Genetics:

A:Gene: S

C:Superfamily: hepatitis B virus surface antigen

C:Keywords: glycoprotein; surface antigen

F:3/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.3%; Score 126; DB 1; Length 226;

Best Local Similarity 91.3%; Pred. No. 1.5e-09;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTAAGTSMFPSCCCTKPTDGN 23

Db 124 CTTAAGNSMFPSCCCTKPTDGN 146

RESULT 14

JQ2045

surface antigen - hepatitis B virus (subtype adw2, strain Len)

C:Species: hepatitis B virus, HBV

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: JQ2045

R:Norder, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus,

J. Gen. Virol. 74, 1341-1348, 1993

A:Title: Genetic relatedness of hepatitis B virus strains of diverse geographical origin

A:Reference number: JQ2044; MUID:93329382; PMID:8336122

A:Contents: Genogroup A

A:Accession: JQ2045

A:Molecule type: DNA

A:Residues: 1-226 <NOR>

C:Genetics:

A:Gene: S

C:Superfamily: hepatitis B virus surface antigen

C:Keywords: surface antigen

Query Match 91.3%; Score 126; DB 2; Length 226;

Best Local Similarity 91.3%; Pred. No. 1.5e-09;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTAAGTSMFPSCCCTKPTDGN 23

Db 124 CTTAAGNSMFPSCCCTKPTDGN 146

RESULT 15

JQ2052

surface antigen - hepatitis B virus (subtype adw2, strain 8903/86)

C:Species: hepatitis B virus, HBV

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: JQ2052

R:Norder, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus,

J. Gen. Virol. 74, 1341-1348, 1993

A:Title: Genetic relatedness of hepatitis B virus strains of diverse geographical origin

A:Reference number: JQ2044; MUID:93329382; PMID:8336122

A:Contents: Genogroup A

A:Accession: JQ2052

A:Molecule type: DNA

A:Residues: 1-226 <NOR>

C:Genetics:

A:Gene: S

C:Superfamily: hepatitis B virus surface antigen

C:Keywords: surface antigen

Query Match 91.3%; Score 126; DB 2; Length 226;

Best Local Similarity 91.3%; Pred. No. 1.5e-09;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTAAGTSMFPSCCCTKPTDGN 23

Db 124 CTTAAGNSMFPSCCCTKPTDGN 146

Search completed: July 26, 2004, 11:29:30

Job time : 3.116 secs

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OM protein - protein search, using sw model

Run on: July 26, 2004, 11:13:24 ; Search time 1.472 Seconds
(without alignments)
813.596 Million cell updates/sec

Title: US-09-719-533A-3_COPY_298_320
Perfect score: 138
Sequence: 1 CTTPAQGTSMFPSCCTCKPTDRN 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	131	94.9	389	1 VMSA_HPBVI	P17397 hepatitis b
2	131	94.9	389	1 VMSA_HPBVO	P17399 hepatitis b
3	127	92.0	226	1 VMSA_HPBVD	P1868 hepatitis b
4	126	91.3	226	1 VMSA_HPBVO	P1873 hepatitis b
5	126	91.3	400	1 VMSA_HPBV2	P03141 hepatitis b
6	126	91.3	400	1 VMSA_HPBV3	P17101 hepatitis b
7	126	91.3	400	1 VMSA_HPBVP	Q02317 hepatitis b
8	125	90.6	389	1 VMSA_HPBVA	P17398 hepatitis b
9	124	89.9	389	1 VMSA_HPBVA	P24025 hepatitis b
10	122	88.4	226	1 VMSA_HPBVS	P1869 hepatitis b
11	121	87.7	226	1 VMSA_HPBVN	P30019 hepatitis b
12	121	87.7	400	1 VMSA_HPBV4	P2934 hepatitis b
13	121	87.7	400	1 VMSA_HPBVR	P03140 hepatitis b
14	120	87.0	389	1 VMSA_HPBVM	P03142 hepatitis b
15	118	85.5	389	1 VMSA_HPBVL	P12911 hepatitis b
16	118	85.5	389	1 VMSA_HPBVT	P03139 hepatitis b
17	113	81.9	400	1 VMSA_HPBVT	Q05496 hepatitis b
18	110	78.7	389	1 VMSA_HPBVY	P03138 hepatitis b
19	70	50.7	428	1 VMSA_HPBGS	P03144 ground squ
20	64	46.4	282	1 VMSA_HPBW6	P11293 woodchuck h
21	64	46.4	431	1 VMSA_HPBW5	P12910 woodchuck h
22	62	44.9	431	1 VMSA_HPBW7	P12909 woodchuck h
23	62	44.9	431	1 VMSA_HPBW8	P06432 woodchuck h
24	62	44.9	431	1 VMSA_HPBW8	P17400 woodchuck h
25	58	42.0	426	1 VMSA_HPBW1	P03143 woodchuck h
26	54	39.1	54	1 MT2_YARLI	P41928 yarrowia li
27	51.5	37.3	251	1 K10A_HUMAN	P60014 homo sapien
28	51	37.0	107	1 YG1Y_YEAST	P53232 saccharomyc
29	50.5	36.6	856	1 POLG_PVYC	P22601 potato viru
30	50.5	36.6	856	1 POLG_PVYO	P22602 potato viru
31	50.5	36.6	3061	1 POLG_PVXU	Q02963 p genome po
32	50.5	36.6	3063	1 POLG_PVYN	P45247 p genome po
33	50.5	36.6	3068	1 POLG_PEMVC	Q01500 p genome po

34 50 36.2 2871 1 FBN1_BOVIN
35 49 35.5 1895 1 WR19_ARATH
36 49 35.5 2871 1 FBN1_HUMAN
37 49 35.5 2871 1 FBN1_MOUSE
38 49 35.5 2871 1 FBN1_PIG
39 48 34.8 162 1 MTCD_TETTH
40 47 34.1 224 1 LB15_ARATH
41 47 34.1 307 1 SG33_DROME
42 47 34.1 630 1 AT94_RAT
43 47 34.1 1399 1 JAK3_MOUSE
44 47 34.1 3066 1 POLG_BCMVN
45 47 34.1 3255 1 POLG_LMVE

ALIGNMENTS

RESULT 1
VMSA_HPBVI STANDARD; PRT; 389 AA.
AC P17397;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw / strain Indonesia/p1DW420).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10412;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Saetoseowignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC -----
CC EMBL; D00331; -; NOT_ANNOTATED_CDS.
DR PIR; I28925; SAVLJ3.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; vmsa; 1.
KW Antigen.
FT PROPEP 1 163 MAJOR SURFACE ANTIGEN.
FT CHAIN 164 389
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 389 AA; 42653 MW; 08079BA34F3B90C0 CRC64;
Query Match 94.9%; Score 131; DB 1; Length 389;
Best Local Similarity 95.7%; Pred. No. 1.9e-11;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTTPAQGTSMFPSCCTCKPTDRN 23
Db 287 CTTPAQGTSMFPSCCTCKPTDGN 309
RESULT 2
VMSA_HPBVO STANDARD; PRT; 389 AA.
ID VMSA_HPBVO
AC P17395; PRT;
DT 01-AUG-1990 (Rel. 15, Created)

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DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw / strain Okinawa/pODW282).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosowignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC -----
DR EMBL; D00330; -; NOT ANNOTATED_CDS.
DR PIR; H28925; SAVLJ2.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 163
FT CHAIN 164 389 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 389 AA; 42408 MW; C8CACODD3A3D84A10 CRC64;
Query Match 94.9%; Score 131; DB 1; Length 389;
Best Local Similarity 95.7%; Pred. No. 1.9e-11;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
D5 287 CTTPAQGTSMFPSCCCTKPTDGN 309
RESULT 3
VMSA_HPBVD
ID VMSA_HPBVD STANDARD; PRT; 226 AA.
AC P31868;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus (subtype ad).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31511;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89143494; PubMed=2465492;
RA Okamoto H., Oni S., Wang Y., Itoh Y., Tsuda F., Tanaka T., Akahane Y.,
RA Miyakawa Y., Mayumi M.;
RT "The loss of subtypic determinants in alleles, d/y or w/r, on
RT hepatitis B surface antigen.";
RL Mol. Immunol. 26:197-205(1989).
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CC -----
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw / strain Okinawa/pODW282).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosowignjo R.I., Imai M.,
RA Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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CC -----
DR EMBL; D00330; -; NOT ANNOTATED_CDS.
DR PIR; H28925; SAVLJ2.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 163
FT CHAIN 164 389 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 389 AA; 42408 MW; C8CACODD3A3D84A10 CRC64;
Query Match 94.9%; Score 131; DB 1; Length 389;
Best Local Similarity 95.7%; Pred. No. 1.9e-11;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
D5 287 CTTPAQGTSMFPSCCCTKPTDGN 309
RESULT 3
VMSA_HPBVD
ID VMSA_HPBVD STANDARD; PRT; 226 AA.
AC P31868;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus (subtype ad).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31511;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89143494; PubMed=2465492;
RA Okamoto H., Oni S., Wang Y., Itoh Y., Tsuda F., Tanaka T., Akahane Y.,
RA Miyakawa Y., Mayumi M.;
RT "The loss of subtypic determinants in alleles, d/y or w/r, on
RT hepatitis B surface antigen.";
RL Mol. Immunol. 26:197-205(1989).
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DR EMBL; M27765; AAA45518.1; -.
DR PIR; PLO053; SAVLAD.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 226 AA; 25348 MW; AFC12BCF3B08DC83 CRC64;
Query Match 92.0%; Score 127; DB 1; Length 226;
Best Local Similarity 91.3%; Pred. No. 4.2e-11;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
D5 124 CTTPAQGTSMFPSCCCTKPTDGN 146
RESULT 4
VMSA_HPBVD
ID VMSA_HPBVD STANDARD; PRT; 226 AA.
AC P31873;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus.
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88297159; PubMed=2841200;
RA Rivkina M.B., Lunin V.G., Mahov A.M., Tikchenenko T.I., Kukain R.A.;
RT "Nucleotide sequence of integrated hepatitis B virus DNA and human
RT flanking regions in the genome of the PLC/PRF/5 cell line.";
RL Gene 64:285-296(1988).
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DR EMBL; M21030; AAA45516.1; -.
DR EMBL; X04820; CAA28506.1; -.
DR PIR; JTO293; SAVLHV.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 226 AA; 25476 MW; BFC4329CF1720600 CRC64;
Query Match 91.3%; Score 126; DB 1; Length 226;
Best Local Similarity 91.3%; Pred. No. 5.8e-11;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
D5 124 CTTPAQGTSMFPSCCCTKPTDGN 146
RESULT 5
VMSA_HPBVD
ID VMSA_HPBVD STANDARD; PRT; 400 AA.
AC P03141;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
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DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw2).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408;
RN [1]
RP SEQUENCE FROM N.A.
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
RN Animal virus genetics, pp.57-70, Academic Press, New York (1980).
RN [2]
RP SEQUENCE OF 175-400 FROM N.A.
RX MEDLINE=79244739; PubMed=471053;
RA Valenzuela P., Gray P., Quiroga M., Zaldivar J., Goodman H.M.,
RN Rutter W.J.;
RT "Nucleotide sequence of the gene coding for the major protein of
FT hepatitis B virus surface antigen.";
RL Nature 280:815-819(1979).
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DR EMBL; X02763; CAA26539.1; -.
DR EMBL; J02205; AAA45524.1; -.
DR PIR; A03706; SAVLVD.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 174 MAJOR SURFACE ANTIGEN.
FT CHAIN 175 400
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 400 AA; 43704 MW; 57356B6293872BC5 CRC64;

Query Match 91.3%; Score 126; DB 1; Length 400;
Best Local Similarity 91.3%; Pred. No. 1e-10;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
||||| |||||||
DB 298 CTTPAQGNMFPSCCCTKPTDGN 320

RESULT 6
VMSA_HPBV9
ID VMSA_HPBV9 STANDARD; PRT; 400 AA.
AC P17101;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw / strain 991).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RA Koehnel H.G., Schueler A., Lottmann S., Thomssen R.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
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DR EMBL; X02763; CAA26539.1; -.
DR EMBL; J02205; AAA45524.1; -.
DR PIR; A03706; SAVLVD.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 174 MAJOR SURFACE ANTIGEN.
FT CHAIN 175 400
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 400 AA; 43704 MW; 57356B6293872BC5 CRC64;

Query Match 91.3%; Score 126; DB 1; Length 400;
Best Local Similarity 91.3%; Pred. No. 1e-10;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
||||| |||||||
DB 298 CTTPAQGNMFPSCCCTKPTDGN 320

RESULT 6
VMSA_HPBV9
ID VMSA_HPBV9 STANDARD; PRT; 400 AA.
AC P17101;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw / strain 991).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RA Koehnel H.G., Schueler A., Lottmann S., Thomssen R.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; X02763; CAA26539.1; -.
DR EMBL; J02205; AAA45524.1; -.
DR PIR; A03706; SAVLVD.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 174 MAJOR SURFACE ANTIGEN.
FT CHAIN 175 400
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 400 AA; 43704 MW; 57356B6293872BC5 CRC64;

Query Match 91.3%; Score 126; DB 1; Length 400;
Best Local Similarity 91.3%; Pred. No. 1e-10;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
||||| |||||||
DB 298 CTTPAQGNMFPSCCCTKPTDGN 320

RESULT 7
VMSA_HPBV9
ID VMSA_HPBV9 STANDARD; PRT; 400 AA.
AC Q02317;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw / strain Philippino/pFDW294).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31514;
RN [1]
RP SEQUENCE FROM N.A.
RA Estacio R.C., Chavez C.C., Okamoto H., Lingao A.L., Reyes M.T.,
RA Domingo E., Mayumi M.;
RT "Nucleotide sequence of a hepatitis B virus genome of subtype adw
RT isolated from a Philippino: comparison with the reported three genomes
RT of the same subtype.";
RL J. Gastroenterol. Hepatol. 3:215-222(1988).
CC -----
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CC -----
DR EMBL; M57663; AAA69680.1; -.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 174 MAJOR SURFACE ANTIGEN.
FT CHAIN 175 400
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 400 AA; 43740 MW; 7EBD53A004136BD2 CRC64;

Query Match 91.3%; Score 126; DB 1; Length 400;
Best Local Similarity 91.3%; Pred. No. 1e-10;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
||||| |||||||
DB 298 CTTPAQGNMFPSCCCTKPTDGN 320
```

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EMBL; M32138; AAA45502.1; --
PIR; B34773; SAVLAR.
InterPro; IPR000349; Hepvir_surfag.
Pfam; PF00695; VMSA; 1.
Antigen.
PROPEP 1 163 MAJOR SURFACE ANTIGEN.
CHAIN 164 389
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 389 AA; 42733 MW; B806D0D4B2B23BF5 CRC64;

Query Match 89.9%; Score 124; DB 1; Length 389;
Best Local Similarity 87.0%; Pred. No. 1.9e-10;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMPSCCTKPTDRN 23
DB 287 CTTPAQGTSMPSCCTKPSDGN 309

RESULT 10
VMSA_HPBVS STANDARD; PRT; 226 AA.
ID_VMSA_HPBVS
AC P31859;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus (subtype ar).
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31516;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89143494; PubMed=2465492;
RA Okamoto H., Omi S., Wang Y., Itoh Y., Tsuda F., Tanaka T., Akahane Y., Miyakawa Y., Mayumi M.;
RT "The loss of subtypic determinants in alleles, d/y or w/r, on hepatitis B surface antigen.";
RL Mol. Immunol. 26:197-205(1989).

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EMBL; M27766; AAA45519.1; --
PIR; PL0056; SAVLAR.
InterPro; IPR000349; Hepvir_surfag.
Pfam; PF00695; VMSA; 1.
Antigen.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 226 AA; 25377 MW; B8DF68F2B823FAF CRC64;

Query Match 88.4%; Score 122; DB 1; Length 226;
Best Local Similarity 87.0%; Pred. No. 2.1e-10;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMPSCCTKPTDRN 23

```

Db      124 CTIPAGTSMFPSCCTKPSDAN 146

RESULT 11
VMSA_HPBVN
ID VMSA_HPBVN STANDARD; PRT; 226 AA.
AC P30019;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus (subtype adr / strain NC-1).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31513;
RN [1]
RP SEQUENCE FROM N.A.
RA Qi Z.H., Yan J., Xiong W.J., Cai L.W.;
RT "Determination of the nucleotide sequence and studies on the
RT structure of hepatitis B virus (HBV) adr NC-1 surface antigen (HBsAg)
RT gene.";
RL Sheng Wu Hua Hsueh Tsa Chih 4:201-209(1988).
DR PIR; JC1002; SAVLN1.
DR InterPro; IPR000349; Hepvir_surfaG.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 226 AA; 25397 MW; 90FC24FA074B66AF CRC64;

Query Match 87.7%; Score 121; DB 1; Length 226;
Best Local Similarity 87.0%; Pred. No. 3e-10;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTIPAGTSMFPSCCTKPTDRN 23
||| ||||| ||||| ||||| |||||
Db      124 CTIPAGTSMFPSCCTKPSDGN 146

RESULT 12
VMSA_HPBV4
ID VMSA_HPBV4 STANDARD; PRT; 400 AA.
AC P12934; Q67860;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adr4).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10409;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8324570; PubMed=6306594;
RA Fujiyama A., Miyanohara A., Nozaki C., Yoneyama T., Ohtomo N.,
RA Matsubara K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr.";
RL Nucleic Acids Res. 11:4601-4610(1983).
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CC -----
DR EMBL; X01587; CAA25747.1; ALT INIT.
DR EMBL; X01587; CAA25743.1; ALT INIT.
DR InterPro; IPR000349; Hepvir_surfaG.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 174

Query Match 87.7%; Score 121; DB 1; Length 400;
Best Local Similarity 87.0%; Pred. No. 5.1e-10;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTIPAGTSMFPSCCTKPTDRN 23
||| ||||| ||||| ||||| |||||
Db      298 CTIPAGTSMFPSCCTKPSDGN 320

RESULT 13
VMSA_HPBVR
ID VMSA_HPBVR STANDARD; PRT; 400 AA.
AC P03140;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adr).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=106820;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adr.";
RL Nucleic Acids Res. 11:1747-1757(1983).
RN [2]
RP SEQUENCE OF 176-350 FROM N.A.
RX MEDLINE=85107103; PubMed=3968537;
RA Takeshima H., Inokoshi J., Namiki M., Shimada J., Omura S.;
RT "Structural analysis of the gene coding for hepatitis B virus surface
RT antigen and its product.";
RL J. Gen. Virol. 66:195-200(1985).
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CC -----
DR EMBL; V00867; CAA24234.1; ALT INIT.
DR PIR; A03705; SAVLA.
DR InterPro; IPR000349; Hepvir_surfaG.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 174
FT CHAIN 175 400 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 400 AA; 43685 MW; 16DB0B15C6CB97A CRC64;

Query Match 87.7%; Score 121; DB 1; Length 400;
Best Local Similarity 87.0%; Pred. No. 5.1e-10;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTIPAGTSMFPSCCTKPTDRN 23
||| ||||| ||||| ||||| |||||
Db      298 CTIPAGTSMFPSCCTKPSDGN 320

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FT CHAIN 175 400 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 400 AA; 43542 MW; 01053BEC24053F9 CRC64;

Query Match 87.7%; Score 121; DB 1; Length 400;
Best Local Similarity 87.0%; Pred. No. 5.1e-10;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTIPAGTSMFPSCCTKPTDRN 23
||| ||||| ||||| ||||| |||||
Db      298 CTIPAGTSMFPSCCTKPSDGN 320

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RESULT 14
VMSA_HPBVL
ID VMSA_HPBVL STANDARD; PRT; 389 AA.
AC P1291;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=106821;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83168919; PubMed=6300776;
RA Ono Y., Onda H., Sasaki R., Igarashi K., Sugino Y., Nishioka K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adw.";
RL Nucleic Acids Res. 11:1747-1757(1983).
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CC -----
DR EMBL; V00866; CAA24233.1; ALT_INIT.
DR PIR; A93460; SAVLVE.
DR InterPro; IPR000349; Hepvir_surfaG.
DR Pfam; PF00695; vMSA; 1.
KW Antigen.
FT PROPEP 1 163 MAJOR SURFACE ANTIGEN.
FT CHAIN 164 389 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 26 26 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 389 AA; 42354 MW; F59EP2E7BEFC58B5 CRC64;

Query Match 87.0%; Score 120; DB 1; Length 389;
Best Local Similarity 87.0%; Pred. No. 6.9e-10;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
DB 287 CTTPAQGNKFPSCCCTKPTDGN 309

RESULT 15
VMSA_HPBVL
ID VMSA_HPBVL STANDARD; PRT; 389 AA.
AC P1291;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (strain lsh / chimpanzee isolate).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258473; PubMed=2838576;
RA Vaudin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
RA Harrison T.J.;
RT "The complete nucleotide sequence of the genome of a hepatitis B
RT virus isolated from a naturally infected chimpanzee.";
RL J. Gen. Virol. 69:1383-1389(1988).
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CC -----
DR EMBL; D00220; BAA00159.1; -.
DR PIR; C28885; SAVLCP.
DR InterPro; IPR000349; Hepvir_surfaG.
DR Pfam; PF00695; vMSA; 1.
KW Antigen.
FT PROPEP 1 163 MAJOR SURFACE ANTIGEN.
FT CHAIN 164 389 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 389 AA; 42539 MW; 87D1F93382A10DBD CRC64;

Query Match 85.5%; Score 118; DB 1; Length 389;
Best Local Similarity 82.6%; Pred. No. 1.3e-09;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
DB 287 CTTPAQGTSLIPSCCCTKPSDGN 309

Search completed: July 26, 2004, 11:27:38
Job time : 1.472 secs
```

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OM protein - protein search, using sw model

Run on: July 26, 2004, 11:22:09 ; Search time 6.072 Seconds
(without alignments)
1195.145 Million cell updates/sec

Title: US-09-719-533A-3_COPY_298_320
Perfect score: 138
Sequence: 1 CTTPAQGTSMFPSCCCTKPTDRN 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	63	12	Q9Q660 hepatitis b
2	138	100.0	228	12	Q9WHR5 hepatitis b
3	133	96.4	42	12	Q80Q6 hepatitis b
4	133	96.4	226	12	Q9WHR2 hepatitis b
5	132	95.7	63	12	Q9Q6D5 hepatitis b
6	132	95.7	226	12	Q80GX4 hepatitis b
7	131	94.9	53	12	Q92942 hepatitis b
8	131	94.9	53	12	Q92943 hepatitis b
9	131	94.9	61	12	Q90258 hepatitis b
10	131	94.9	63	12	Q9Q678 hepatitis b
11	131	94.9	63	12	Q9Q6C5 hepatitis b
12	131	94.9	63	12	Q9Q6A0 hepatitis b
13	131	94.9	63	12	Q9Q6B5 hepatitis b
14	131	94.9	63	12	Q9Q692 hepatitis b
15	131	94.9	63	12	Q9Q664 hepatitis b
16	131	94.9	63	12	Q9Q668 hepatitis b

17	131	94.9	63	12	Q9Q686 hepatitis b
18	131	94.9	63	12	Q9Q6D6 hepatitis b
19	131	94.9	63	12	Q9Q671 hepatitis b
20	131	94.9	63	12	Q9Q666 hepatitis b
21	131	94.9	63	12	Q9Q662 hepatitis b
22	131	94.9	63	12	Q9Q663 hepatitis b
23	131	94.9	63	12	Q9Q6B9 hepatitis b
24	131	94.9	63	12	Q9Q6A4 hepatitis b
25	131	94.9	63	12	Q9Q683 hepatitis b
26	131	94.9	63	12	Q9Q6A1 hepatitis b
27	131	94.9	63	12	Q9Q689 hepatitis b
28	131	94.9	63	12	Q9Q681 hepatitis b
29	131	94.9	63	12	Q9Q659 hepatitis b
30	131	94.9	63	12	Q9Q6B7 hepatitis b
31	131	94.9	63	12	Q9Q676 hepatitis b
32	131	94.9	63	12	Q9Q6C3 hepatitis b
33	131	94.9	63	12	Q9Q672 hepatitis b
34	131	94.9	63	12	Q9Q679 hepatitis b
35	131	94.9	63	12	Q9Q674 hepatitis b
36	131	94.9	63	12	Q9Q6B6 hepatitis b
37	131	94.9	63	12	Q9Q685 hepatitis b
38	131	94.9	63	12	Q9Q680 hepatitis b
39	131	94.9	63	12	Q9Q658 hepatitis b
40	131	94.9	63	12	Q9Q6B0 hepatitis b
41	131	94.9	63	12	Q9Q693 hepatitis b
42	131	94.9	63	12	Q9Q6C9 hepatitis b
43	131	94.9	63	12	Q9Q6C0 hepatitis b
44	131	94.9	63	12	Q9Q6C1 hepatitis b
45	131	94.9	63	12	Q9Q684 hepatitis b

ALIGNMENTS

RESULT 1

Q9Q660 PRELIMINARY; PRT; 63 AA.
ID Q9Q660
AC Q9Q660;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DE Major surface antigen (Fragment).
CS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCN41;
RA Xia G.-L., Nainan O.V., Jia Z.-Y., Cao H.-L., Liu C.-B.,
RA Margolis H.S.;
RT "Distribution of hepatitis B virus subtypes and genotypes in China."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF198767; AAF15686.1; -
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfaG.
DR DR Pfam; PF00695; VMGA; 1.
KW Antigen.
FT NON_TER 1 1
FT NON_TER 63 63
SQ SEQUENCE 63 AA; 6958 MW; F3E1D919C4CF96C7 CRC64;

Query Match 100.0%; Score 138; DB 12; Length 63;
Best Local Similarity 100.0%; Pred. No. 7.8e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||||
DB 11 CTTPAQGTSMFPSCCCTKPTDRN 33
|||||

RESULT 2

Q9WHR5 PRELIMINARY; PRT; 228 AA.
ID Q9WHR5

```
AC Q9WHR5;
DC 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Major surface antigen.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TSN;
RA Ireland J., Kean J., O'Donnell B., Basuni A.A., Wallace L.A.,
RA Carman W.F., Lau G.K.K.;
RT "Reactivity of in vitro expressed hepatitis B surface antigen variants
RT in commercial diagnostic assays.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF134137; AAD31854.1; -
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 228 AA; 25717 MW; DFA7647E96F789AB CRC64;

Query Match 100.0%; Score 138; DB 12; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||
Db 126 CTTPAQGTSMFPSCCCTKPTDRN 148

RESULT 3
Q90QQ6
ID Q80QQ6 PRELIMINARY; PRT; 42 AA.
AC Q80QQ6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface antigen (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA;
RA Zoellner B.;
RT "Natural variations between HBV genotypes A and D.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY184122; AAO40321.1; -
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4343 MW; A8213F18209B6B29 CRC64;

Query Match 96.4%; Score 133; DB 12; Length 42;
Best Local Similarity 95.7%; Pred. No. 3.4e-14;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||
Db 11 CTTPAQGTSMFPSCCCTKPTDRN 33

RESULT 4
Q9WHR2
ID Q9WHR2 PRELIMINARY; PRT; 226 AA.
AC Q9WHR2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Major surface antigen.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
```

```
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ARG145;
RA Ireland J., Kean J., O'Donnell B., Basuni A.A., Wallace L.A.,
RA Carman W.F., Lau G.K.K.;
RT "Reactivity of in vitro expressed hepatitis B surface antigen variants
RT in commercial diagnostic assays.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF134134; AAD31851.1; -
DR PIR; JQ2045; JQ2045.
DR PIR; JQ2045; JQ2046.
DR PIR; JQ2047; JQ2047.
DR PIR; JQ2048; JQ2048.
DR PIR; JQ2050; JQ2050.
DR PIR; JQ2051; JQ2051.
DR PIR; JQ2053; JQ2053.
DR PIR; JQ2054; JQ2054.
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 226 AA; 25493 MW; 898F1C48865EA26C CRC64;

Query Match 96.4%; Score 133; DB 12; Length 226;
Best Local Similarity 95.7%; Pred. No. 1.7e-13;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||
Db 124 CTTPAQGTSMFPSCCCTKPTDRN 146

RESULT 5
Q90Q6D5
ID Q90Q6D5 PRELIMINARY; PRT; 63 AA.
AC Q90Q6D5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Major surface antigen (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHN7;
RA Xia G.-L., Nainan O.V., Jia Z.-Y., Cao H.-L., Liu C.-B.,
RA Margolis H.S.;
RT "Distribution of hepatitis B virus subtypes and genotypes in China.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF198692; AAF15611.1; -
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER 1
FT NON_TER 63
SQ SEQUENCE 63 AA; 6901 MW; 2F7C1019C4CF8548 CRC64;

Query Match 95.7%; Score 132; DB 12; Length 63;
Best Local Similarity 95.7%; Pred. No. 7.3e-14;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDRN 23
|||
Db 11 CTTPAQGTSMFPSCCCTKPTDRN 33

RESULT 6
Q80GX4
ID Q80GX4 PRELIMINARY; PRT; 226 AA.
AC Q80GX4;
```

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE S protein.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FMU016;
RA Lin X., Zheng D.L., Xu X.;
RT "Genotype distribution of HBV from hepatocellular carcinoma tissues.";
RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY063837; AAP06615.1; -
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; VMSA; 1.
SQ SEQUENCE 226 AA; 25463 MW; E639CFF4F914C2CB CRC64;

Query Match 95.7%; Score 132; DB 12; Length 226;
Best Local Similarity 95.7%; Pred. No. 2.4e-13;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
|||||
Db 124 CTTPAQGTSMFPSCCCTKPTDAN 146
|||||

RESULT 7
O92942 PRELIMINARY; PRT; 53 AA.
ID O92942;
AC O92942;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface antigen a-determinant (Major surface antigen)
DE (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Philippine H63;
RA Cajimat M.N., Santiago M.L., Vinculato F.A., Hafalla J.C., Dizon F.A.;
RT "Genetic diversity of the Hepatitis B virus surface antigen (HBsAg) a-determinant among Filipino blood donors.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF050309; AAC05550.1; -
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER 1 53
FT NON_TER 53
SQ SEQUENCE 53 AA; 5366 MW; B20F45572E8749CB CRC64;

Query Match 94.9%; Score 131; DB 12; Length 53;
Best Local Similarity 95.7%; Pred. No. 8.9e-14;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
|||||
Db 20 CTTPAQGTSMFPSCCCTKPTDGN 42
|||||

RESULT 8
O92943 PRELIMINARY; PRT; 53 AA.
ID O92943;
AC O92943;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface antigen a-determinant (Major surface antigen)

DE (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Philippine H64;
RA Cajimat M.N., Santiago M.L., Vinculato F.A., Hafalla J.C., Dizon F.A.;
RT "Genetic diversity of the Hepatitis B virus surface antigen (HBsAg) a-determinant among Filipino blood donors.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF050310; AAC05551.1; -
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER 1 53
FT NON_TER 53
SQ SEQUENCE 53 AA; 5366 MW; B20F45572E8749CB CRC64;

Query Match 94.9%; Score 131; DB 12; Length 53;
Best Local Similarity 95.7%; Pred. No. 8.9e-14;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
|||||
Db 20 CTTPAQGTSMFPSCCCTKPTDGN 42
|||||

RESULT 9
O90258 PRELIMINARY; PRT; 61 AA.
ID O90258;
AC O90258;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Major surface antigen (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P-150;
RA MEDLINE=98437477; PubMed=9763505;
RA Povorawan Y., Theamboonlers A., Chongsrisawat V., Sarpavat S.;
RT "Molecular analysis of the a determinant of HBsAg in children of HBeAg-positive mothers upon failure of postexposure prophylaxis.";
RL Int. J. Infect. Dis. 2:216-220(1998).
DR EMBL; AF074438; AAD13366.1; -
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT NON_TER 1 61
FT NON_TER 61
SQ SEQUENCE 61 AA; 6527 MW; 46B7BA27BB500EEB CRC64;

Query Match 94.9%; Score 131; DB 12; Length 61;
Best Local Similarity 95.7%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
|||||
Db 15 CTTPAQGTSMFPSCCCTKPTDGN 37
|||||

RESULT 10
O90678 PRELIMINARY; PRT; 63 AA.
ID O90678;
AC O90678;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Major surface antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCN39;
 RA Xia G.-L., Nainan O.V., Jia Z.-Y., Cao H.-L., Liu C.-B.,
 RA Margolis H.S.;
 RT "Distribution of hepatitis B virus subtypes and genotypes in China."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF198749; AAF15668.1; -
 DR GO; GO:0016032; P:Viral life cycle; IEA.
 DR InterPro; IPR000349; Hepvir_surfa.
 DR Pfam; PF00695; vmsa; 1.
 KW Antigen.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 63 AA; 6859 MW; 853AA919C4CF96D3 CRC64;

Query Match 94.9%; Score 131; DB 12; Length 63;
 Best Local Similarity 95.7%; Pred. No. 1.1e-13;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 DB 11 CTTPAQGTSMFPSCCCTKPTDGN 33

RESULT 11

Q9Q6C5
 ID Q9Q6C5 PRELIMINARY; PRT; 63 AA.
 AC Q9Q6C5
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Major surface antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCN61;
 RA Xia G.-L., Nainan O.V., Jia Z.-Y., Cao H.-L., Liu C.-B.,
 RA Margolis H.S.;
 RT "Distribution of hepatitis B virus subtypes and genotypes in China."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF198702; AAF15621.1; -
 DR GO; GO:0016032; P:Viral life cycle; IEA.
 DR InterPro; IPR000349; Hepvir_surfa.
 DR Pfam; PF00695; vmsa; 1.
 KW Antigen.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 63 AA; 6859 MW; 853AA919C4CF96D3 CRC64;

Query Match 94.9%; Score 131; DB 12; Length 63;
 Best Local Similarity 95.7%; Pred. No. 1.1e-13;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 DB 11 CTTPAQGTSMFPSCCCTKPTDGN 33

RESULT 12

Q9Q6A0
 ID Q9Q6A0 PRELIMINARY; PRT; 63 AA.
 AC Q9Q6A0
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Major surface antigen (Fragment)

OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCN71;
 RA Xia G.-L., Nainan O.V., Jia Z.-Y., Cao H.-L., Liu C.-B.,
 RA Margolis H.S.;
 RT "Distribution of hepatitis B virus subtypes and genotypes in China."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF198727; AAF15646.1; -
 DR GO; GO:0016032; P:Viral life cycle; IEA.
 DR InterPro; IPR000349; Hepvir_surfa.
 DR Pfam; PF00695; vmsa; 1.
 KW Antigen.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 63 AA; 6859 MW; 853AA919C4CF96D3 CRC64;

Query Match 94.9%; Score 131; DB 12; Length 63;
 Best Local Similarity 95.7%; Pred. No. 1.1e-13;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 DB 11 CTTPAQGTSMFPSCCCTKPTDGN 33

RESULT 13

Q9Q6B5
 ID Q9Q6B5 PRELIMINARY; PRT; 63 AA.
 AC Q9Q6B5
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Major surface antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CC70;
 RA Xia G.-L., Nainan O.V., Jia Z.-Y., Cao H.-L., Liu C.-B.,
 RA Margolis H.S.;
 RT "Distribution of hepatitis B virus subtypes and genotypes in China."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF198712; AAF15631.1; -
 DR GO; GO:0016032; P:Viral life cycle; IEA.
 DR InterPro; IPR000349; Hepvir_surfa.
 DR Pfam; PF00695; vmsa; 1.
 KW Antigen.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 63 AA; 6859 MW; 853AA919C4CF96D3 CRC64;

Query Match 94.9%; Score 131; DB 12; Length 63;
 Best Local Similarity 95.7%; Pred. No. 1.1e-13;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTPAQGTSMFPSCCCTKPTDGN 23
 DB 11 CTTPAQGTSMFPSCCCTKPTDGN 33

RESULT 14

Q9Q692
 ID Q9Q692 PRELIMINARY; PRT; 63 AA.
 AC Q9Q692
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Major surface antigen (Fragment).

Qy	1	CTTPAQGTSMPSCCCKPTDRN	23
Db	11	CTTPAQGTSMPSCCCKPTDGN	33

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Search completed: July 26, 2004, 11:28:57
Job time : 7.072 secs
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OM protein - protein search, using sw model

Run on: July 26, 2004, 11:12:29 ; Search time 88.076 Seconds

(without alignments)
728.215 Million cell updates/sec

Title: US-09-719-533A-3_COPY_174_400

Perfect score: 1281

Sequence: 1 NMENIAGLLGLLVLAGF.....NILSPFMLPIPFCLWYI 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A: Geneseqp_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	1281	100.0	400	3	AAY44349 Human hep
2	1235	96.4	400	4	AAG66929 HBV genot
3	1213	94.7	228	2	AAR67368 Mutant He
4	1194	93.2	228	2	AAR67369 Mutant He
5	1190	92.9	281	4	AAE04620 HBsAg pre
6	1190	92.9	389	2	AAR55287 Deduced s
7	1187	92.7	281	5	AAM52693 Hepatitis
8	1187	92.7	387	2	AAR10852 Modified
9	1187	92.7	388	2	AAR10851 Modified
10	1187	92.7	389	5	AAM52682 Hepatitis
11	1187	92.7	424	2	AAR37797 RTS* prot
12	1187	92.7	424	2	AAR37796 RTS prote
13	1185	92.5	400	4	AAG66928 HBV genot
14	1185	92.5	531	4	AAE04622 Chimeric
15	1184	92.4	226	2	AAK33252 Deduced s
16	1184	92.4	226	2	AAK33252 Deduced s
17	1184	92.4	251	2	AAE04621 Chimeric
18	1184	92.4	390	4	AAE04621 Chimeric
19	1181	92.2	226	5	AAM52694 Hepatitis
20	1181	92.2	280	2	AAR10850 Modified
21	1178	92.0	226	1	AAK30096 Sequence
22	1178	92.0	226	1	AAK30060 Surface a
23	1178	92.0	226	1	AAK30023 Sequence a
24	1178	92.0	226	1	AAK80417 Sequence
25	1178	92.0	226	3	AAK35766 Peptidyl

26 1178 92.0 226 4 AAB98041 Hepatitis
27 1178 92.0 226 4 AAB80956 Aab80956 Viral pro
28 1178 92.0 226 5 AAB05219 Hepatitis
29 1178 92.0 226 5 AAU97646 Hepatitis
30 1178 92.0 229 6 ABP55076 Hepatitis
31 1178 92.0 281 1 AAP60561 Hepatitis
32 1178 92.0 347 3 AAB10596 HBV fusio
33 1178 92.0 389 4 AAG62931 Amino aci
34 1173 91.6 281 2 AAK55281 Deduced s
35 1172 91.5 226 4 AAG62930 Amino aci
36 1172 91.5 250 2 AAR11496 Aar11496 RPI42/HBS
37 1166 91.0 281 1 AAP60163 Subtype a
38 1166 91.0 281 1 AAP60560 Hepatitis
39 1166 91.0 281 1 AAP60617 C-termina
40 1166 91.0 318 2 AAR60174 Chimeric
41 1166 91.0 383 1 AAP60416 Sequence
42 1166 91.0 385 2 AAR60176 Chimeric
43 1166 91.0 582 7 ADD69670 Chimeric
44 1166 91.0 590 7 ADD69668 Chimeric
45 1166 91.0 658 7 ADD69666 Chimeric

ALIGNMENTS

RESULT 1
AAY44349
ID AAY44349 standard; protein; 400 AA.
XX AAY44349;
XX
XX
DT 06-AUG-2003 (revised)
DT 14-MAR-2000 (first entry)
XX
XX Human hepatitis B virus large surface antigen.
XX
XX HBIG; Hepatitis B immunoglobulin; HBV; Hepatitis B virus;
KW large surface antigen; mutant major surface antigen; HBV infection;
KW human hepatitis B virus; hepatocellular carcinoma;
KW human hepatitis B virus surface antigen- 'S'- 145 Singapore strain.
XX
XX Hepatitis B virus.
XX
XX Key Location/Qualifiers
FH Misc-difference 123..400
FT FT /note= "No corresponding nucleotides in SEQ ID NO:1"
XX
XX WO9966047-A1.
XX
XX 23-DEC-1999.
XX
XX 19-JUN-1998; 98WO-SG000045.
XX
XX 19-JUN-1998; 98WO-SG000045.
XX
XX (GOVE-) GOVERNMENT REPUBLIC SINGAPORE.
XX
XX Oon CJ, Lim GK, Leong AL, Zhao Y, Chen WN;
XX WPI; 2000-106103/09.
XX N-PSDB; AAZ29453.
XX
XX New vaccine-escape mutant of hepatitis B virus and related proteins,
XX nucleic acids and antibodies, useful for diagnosis, prevention and
XX treatment.
XX
XX Claim 9; Fig 5; 65pp; English.
XX
XX The present sequence is the large surface antigen deduced from the mutant
XX human hepatitis B viral genome. This was isolated from a male, 11 year
XX old Singaporean child which had received standard HBIG and HB vaccine and
XX was infected with the mutated strain designated human hepatitis B virus
XX surface antigen- 'S'- 145 Singapore strain a year later. This protein can

CC be produced by recombinant technology and used in developing polyclonal
 CC or monoclonal antibodies and as a source of diagnostic oligonucleotides.
 CC The mutated major surface antigen is used to raise specific antibodies,
 CC to identify specific binding agents and, in vaccines or compositions for
 CC treatment or prevention of HBV infection and hepatocellular carcinoma.
 CC Antibodies are used in diagnosis or for screening donated body fluids or
 CC tissues. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 400 AA;

Query Match 100.0%; Score 1281; DB 3; Length 400;
 Best Local Similarity 100.0%; Pred. No. 2e-110;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NMENIASGLGLPVLVLAQGFLLTKILTIPOSLSWMTSLNPLGPTVCLGQNSQSISS 60
 DB 174 NMENIASGLGLPVLVLAQGFLLTKILTIPOSLSWMTSLNPLGPTVCLGQNSQSISS 233
 QY 61 HSPTCCPPIPCGYRMWCLRRFIFLCILLCLIFLLVLLDYQGMLPVCPLIPGSTTTSTG 120
 DB 234 HSPTCCPPIPCGYRMWCLRRFIFLCILLCLIFLLVLLDYQGMLPVCPLIPGSTTTSTG 293
 QY 121 PKTCTTTPAQTSMFPSCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLPF 180
 DB 294 PKTCTTTPAQTSMFPSCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLPF 353
 QY 181 VQFVGLSPTVWLSVINWFWGSPSLNLSPPFPELLPIPFCLWYI 227
 DB 354 VQFVGLSPTVWLSVINWFWGSPSLNLSPPFPELLPIPFCLWYI 400

RESULT 2

AA666929
 ID AAG66929 standard; protein; 400 AA.
 AC AAG66929;
 XX
 DT 19-OCT-2001 (first entry)
 XX
 DE HBV genotype B preS1/preS2/HBsAg polypeptide.
 XX
 KW Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBs; HBx; HBp1;
 KW HBsAg; antiviral; vaccine; genotype G; genotyping; HBcAg; HBsAg.
 XX
 OS Hepatitis B virus.
 XX
 FN WO200140279-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 20-NOV-2000; 2000WO-EP011526.
 XX
 PR 03-DEC-1999; 99EP-00870252.
 PR 07-DEC-1999; 99US-0169287P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 XX Stuyver L, Van Geyt C, De Gendt S;
 XX WPI; 2001-374785/39.
 XX
 XX Novel isolated and/or purified hepatitis B virus polypeptide and
 XX polynucleotide sequences that are phylogenetically different from HBV
 XX genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
 XX therapy.
 XX
 XX Example 3; Fig 6; 94pp; English.

XX The invention relates to the complete nucleic acid sequence of a new
 XX human hepatitis B virus (HBV) genotype, provisionally named genotype G.
 XX This genotype was found with a high prevalence in patients chronically
 XX infected with HBV and residing in Europe and the USA. The invention
 XX relates to a fully defined sequence of 3248 nucleotides as given in

CC specification, a sequence with 92% identity to the given sequence, or
 CC sequence that is degenerate to the mentioned sequences. These
 CC polynucleotides are useful for HBV genotyping. The proteins encoded by
 CC the polynucleotides are useful for detecting antibodies in a biological
 CC sample. Ligands that bind to the proteins and antibodies directed against
 CC the proteins are useful for detecting the proteins and for detecting
 CC HBcAg and HBsAg (precore precursor proteins). They are also useful for
 CC preparing a vaccine or medicament for treating HBV infections. The
 CC present sequence is provided in an amino acid sequence alignment of the
 CC preS1, preS2 and HBsAg open reading frame of the different HBV genotypes
 XX
 SQ Sequence 400 AA;

Query Match 96.4%; Score 1235; DB 4; Length 400;
 Best Local Similarity 96.9%; Pred. No. 3.6e-106;
 Matches 220; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 NMENIASGLGLPVLVLAQGFLLTKILTIPOSLSWMTSLNPLGPTVCLGQNSQSISS 60
 DB 174 NMENIASGLGLPVLVLAQGFLLTKILTIPOSLSWMTSLNPLGPTVCLGQNSQSISS 233
 QY 61 HSPTCCPPIPCGYRMWCLRRFIFLCILLCLIFLLVLLDYQGMLPVCPLIPGSTTTSTG 120
 DB 234 HSPTCCPPIPCGYRMWCLRRFIFLCILLCLIFLLVLLDYQGMLPVCPLIPGSTTTSTG 293
 QY 121 PKTCTTTPAQTSMFPSCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLPF 180
 DB 294 PKTCTTTPAQTSMFPSCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLPF 353
 QY 181 VQFVGLSPTVWLSVINWFWGSPSLNLSPPFPELLPIPFCLWYI 227
 DB 354 VQFVGLSPTVWLSVINWFWGSPSLNLSPPFPELLPIPFCLWYI 400

RESULT 3

AA67368
 ID AAR67368 standard; protein; 228 AA.
 XX
 AC AAR67368;
 XX
 DT 25-MAR-2003 (revised)
 DT 22-SEP-1995 (first entry)
 XX
 DE Mutant Hepatitis B virus surface antigen sequence.
 XX
 KW Hepatitis B virus; HBV; mutant; detection; surface antigen; HBsAg;
 KW detection; vaccine; diagnostic; prognosis; therapy.
 XX
 OS Hepatitis B virus.
 XX
 FH Key Location/Qualifiers
 FT Region 123..124
 FT /note= "Dipeptide encoded by insertion sequence."
 XX
 PN WO9426904-A1.
 XX
 PD 24-NOV-1994.
 XX
 PF 09-MAY-1994; 94WO-US005090.
 XX
 PR 07-MAY-1993; 93US-00059031.
 XX
 PA (ABBO) ABBOTT LAB.
 PA (UNIU) UNIV GLASGOW.
 XX
 XX Carman W, Decker RH, Wallace L, Mimms LT, Solomon LR;
 XX WPI; 1995-006799/01.
 DR N-PSDB; AAQ75318.
 XX
 XX New mutant hepatitis B virus polynucleotide - used to develop prods. for
 XX diagnosis, prognosis, therapy and studies involving hepatitis B
 XX infection.

XX Example 2; Page 49-50; 59pp; English.

XX The mutant hepatitis B virus (HBV) polypeptide comprises an insertion of two amino acid residues at position 122 of the HBV surface antigen (HBsAg). The polynucleotide encoding the mutant polypeptide can be used for detection of mutant HBV and for the production of the polypeptide which can be used in vaccines for the treatment of infection. Antibodies against such polypeptides can be used for detecting the mutant HBV antigen. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 228 AA;

Query Match 94.7%; Score 1213; DB 2; Length 228;
 Best Local Similarity 94.3%; Pred. No. 2.2e-104;
 Matches 215; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

QY 2 MENIASGLGLPLVLQAGFFLLTKILTIPOSLDSWNTSLNFGGPTVCLGNSQSQISSH 61
 DB 1 MENTTSGLLGLPLVLQAGFFLLTKILTIPOSLDSWNTSLNFGGPTVCLGNSQSQISSH 60

QY 62 SPTCCPPICPGVRWMCRLRRFIIFLCILLCLIFLLVLDYOGMLPVCPLIPGSTTTSTGP 121
 DB 61 SPTCCPPICPGVRWMCRLRRFIIFLCILLCLIFLLVLDYOGMLPVCPLIPGSTTTSTGP 120

QY 122 CK--TCTTPAQGTSMPFSCCCTKPTDRNCTCIPSSWAFKYLMEWASVRFSLSLVLP 179
 DB 121 CRNTTCTTPAQGTSMPFSCCCTKPTDRNCTCIPSSWAFKYLMEWASVRFSLSLVLP 180

QY 180 FVQWFVGLSPTVWLSVINMMWYGPGLYNILSPFPLPIPFCLWVYI 227
 DB 181 FVQWFVGLSPTVWLSVINMMWYGPGLYNILSPFPLPIPFCLWVYI 228

RESULT 4

AAE02620

ID AAE02620 standard; protein; 228 AA.

XX AC AAE02620;

XX DT 25-MAR-2003 (revised)

XX DT 22-SEP-1995 (first entry)

XX DE Mutant Hepatitis B virus surface antigen sequence.

XX KW Hepatitis B virus; HBV; mutant; detection; surface antigen; HBsAg; detection; vaccine; diagnostic; prognosis; therapy.

XX OS Hepatitis B virus.

XX FH Key Location/Qualifiers

FT Region 123..124

FT /note= "Dipeptide encoded by insertion sequence."

XX PN WO9426904-A1.

XX PD 24-NOV-1994.

XX PF 09-MAY-1994; 94WO-US005090.

XX PR 07-MAY-1993; 93US-00059031.

XX PA (ABBO) ASBOTI LAB.

XX PA (UNIU) UNIV GLASGOW.

XX PI Carman W, Decker RH, Wallace L, Mimms LT, Solomon LR;

XX WPI; 1995-006799/01.

XX DR New mutant hepatitis B virus polynucleotide - used to develop prods. for diagnosis, prognosis, therapy and studies involving hepatitis B infection.

XX PT

PS Example 2; Page 50-51; 59pp; English.

XX The mutant hepatitis B virus (HBV) polypeptide comprises an insertion of two amino acid residues at position 122 of the HBV surface antigen (HBsAg). The polynucleotide encoding the mutant polypeptide can be used for detection of mutant HBV and for the production of the polypeptide which can be used in vaccines for the treatment of infection. Antibodies against such polypeptides can be used for detecting the mutant HBV antigen. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 228 AA;

Query Match 93.2%; Score 1194; DB 2; Length 228;
 Best Local Similarity 92.1%; Pred. No. 1.3e-102;
 Matches 210; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 2 MENIASGLGLPLVLQAGFFLLTKILTIPOSLDSWNTSLNFGGPTVCLGNSQSQISSH 61
 DB 1 MENTTSGLLGLPLVLQAGFFLLTKILTIPOSLDSWNTSLNFGGPTVCLGNSQSQISSH 60

QY 62 SPTCCPPICPGVRWMCRLRRFIIFLCILLCLIFLLVLDYOGMLPVCPLIPGSTTTSTGP 121
 DB 61 SPTCCPPICPGVRWMCRLRRFIIFLCILLCLIFLLVLDYOGMLPVCPLIPGSTTTSTGP 120

QY 122 CK--TCTTPAQGTSMPFSCCCTKPTDRNCTCIPSSWAFKYLMEWASVRFSLSLVLP 179
 DB 121 CRNTTCTTPAQGTSMPFSCCCTKPTDRNCTCIPSSWAFKYLMEWASVRFSLSLVLP 180

QY 180 FVQWFVGLSPTVWLSVINMMWYGPGLYNILSPFPLPIPFCLWVYI 227
 DB 181 FVQWFVGLSPTVWLSVINMMWYGPGLYNILSPFPLPIPFCLWVYI 228

RESULT 5

AAE02620

ID AAE02620 standard; protein; 281 AA.

XX AC AAE02620;

XX DT 06-AUG-2001 (first entry)

XX DE HBsAg preS2-S domains encoded by plasmid pCMVII-PS2-SAg.

XX KW Virus-like particle; immunogen; hepatitis B virus surface antigen; HBsAg; HBV; chimeric antigen; hepatitis C virus; HCV; virucide; vaccine; plasmid pCMVII-PS2-SAg; preS2 domain; S domain.

XX OS Hepatitis B virus.

XX FH Key Location/Qualifiers

FT Domain 1..55

FT /label= HBsAg_preS2_domain

FT Domain 56..281

FT /label= HBsAg_S_domain

XX PN WO200138358-A2.

XX PD 31-MAY-2001.

XX PF 22-NOV-2000; 2000WO-US032249.

XX PR 24-NOV-1999; 99US-0167224P.

XX PA (CHIR) CHIRON CORP.

XX PI Selby M, Glazer E, Houghton M;

XX WPI; 2001-367661/38.

XX DR N-PSDB; AAD06731.

XX PT Virus-like particle for use as an immunogen, comprising a first hepatitis B virus surface antigen (HBsAg) and chimeric antigen comprising a second HBsAg covalently linked to hepatitis C immunogenic polypeptide.

XX Example 2; Fig 2; 115pp; English.

XX The invention relates to a virus-like particle for use as an immunogen, comprising a first hepatitis B virus surface antigen (HBsAg) and a chimeric antigen comprising a second HBsAg which is covalently linked to an hepatitis C virus (HCV) immunogenic polypeptide, where the first and the second HBsAg each comprise a substantially complete S domain. The virus-like particle is useful as immunogen and as vaccine. The present sequence consists of preS2 and S domains of HBsAg encoded by plasmid pCMVII-PS2-SAg

XX Sequence 281 AA;

Query Match 92.9%; Score 1190; DB 4; Length 281;

Best Local Similarity 92.5%; Pred. No. 3.7e-102;

Matches 210; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 N N E N I A S G L G P L L V L Q A G F F L L T K I L T I P O S L D S W M T S L N F L G S P V C L G Q N S Q S I S S 60

DB 55 N N E N I T S F L G P L L V L Q A G F F L L T R I L T I P O S L D S W M T S L N F L G S P V C L G Q N S Q S P T S N 114

QY 61 H S P T C C P I C P G Y R W M C L R R F I F L C I L L C L I F L L V L L D Y Q G M L P V C P L I P G S T T T S T G 120

DB 115 H S P T C C P I C P G Y R W M C L R R F I F L C I L L C L I F L L V L L D Y Q G M L P V C P L I P G S T T T S T G 174

QY 121 P C K T C T T P A Q G T S M F P S C C C T K P T D R N C T C I P I P S S W A F A K Y L W E M A S V R F S W L S L L V P F 180

DB 175 P C K T C T T P A Q G S M F P S C C C T K P T D G N C T C I P I P S S W A F A K Y L W E M A S V R F S W L S L L V P F 234

QY 181 V Q W F V G L S P T V L S V I W M W F W G S L Y N I L S P F M P L L P I F F C L W Y I 227

DB 235 V Q W F V G L S P T V L S A I W M W Y G P S L Y S I V S P F I P L L P I F F C L W Y I 281

RESULT 6

AAR55287

ID AAR55287 standard; protein; 389 AA.

AC AAR55287;

DT 25-MAR-2003 (revised)

DT 02-JAN-1995 (first entry)

XX Deduced sequence of HBV surface antigen LS.

XX Surface antigen; recombinant replicable vaccinia virus; hepatitis;

KW prevention; therapy; epitope; hepatitis B virus.

XX Hepatitis B virus.

XX WO9412617-A1.

PN 09-JUN-1994.

XX 24-NOV-1993; 93WO-US011474.

XX 25-NOV-1992; 92US-00982211.

XX (ITBI-) INT BIOTECHNOLOGY LAB INC.

XX Souw Pts, Okeefe RW, Lewis T, Bernstein EG;

XX WPI; 1994-200247/24.

DR N-PSDB; AAR67970.

XX Prevention and treatment of hepatitis - using recombinant replicable vaccinia viruses contg. hepatitis B virus surface and core antigen nucleotide sequences.

PT Example; Fig 22; 252pp; English.

XX The HBV genome (subtype adw) is contained in plasmid pAM6. The 3' end of

CC the ORF coding for the three surface Ags was manipulated to generate pro

CC -02 which contains an intact ORF capable of encoding LS, MS and S Ags.

CC The DNA sequences encoding S, MS and LS were sub- cloned and sequenced.

CC The sequences of the LS are AAR67970/R55287; the sequences of MS are in AAR67961/R55281 and the sequences of S are AAR67962/R55282. Changes in nucleotide and deduced AA sequences from the published sequence are believed to result from variability within the adw subtype. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 389 AA;

Query Match 92.9%; Score 1190; DB 2; Length 389;

Best Local Similarity 92.5%; Pred. No. 5.2e-102;

Matches 210; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 N N E N I A S G L G P L L V L Q A G F F L L T K I L T I P O S L D S W M T S L N F L G S P V C L G Q N S Q S I S S 60

DB 163 N N E N I T S F L G P L L V L Q A G F F L L T R I L T I P O S L D S W M T S L N F L G S P V C L G Q N S Q S P T S N 222

QY 61 H S P T C C P I C P G Y R W M C L R R F I F L C I L L C L I F L L V L L D Y Q G M L P V C P L I P G S T T T S T G 120

DB 223 H S P T C C P I C P G Y R W M C L R R F I F L C I L L C L I F L L V L L D Y Q G M L P V C P L I P G S T T T S T G 282

QY 121 P C K T C T T P A Q G T S M F P S C C C T K P T D R N C T C I P I P S S W A F A K Y L W E M A S V R F S W L S L L V P F 180

DB 283 P C K T C T T P A Q G S M F P S C C C T K P T D G N C T C I P I P S S W A F A K Y L W E M A S V R F S W L S L L V P F 342

QY 181 V Q W F V G L S P T V L S V I W M W F W G S L Y N I L S P F M P L L P I F F C L W Y I 227

DB 343 V Q W F V G L S P T V L S A I W M W Y G P S L Y S I V S P F I P L L P I F F C L W Y I 389

RESULT 7

AAM52693

ID AAM52693 standard; protein; 281 AA.

AC AAM52693;

XX 26-FEB-2002 (first entry)

DT Hepatitis B virus surface antigen M protein.

DE HBV; S protein; major surface protein; M protein; surface antigen; HBsAg;

KW yeast; coexpression; fusion protein; epitope; antiviral; antiparasitic;

KW vaccine; mixed composition.

XX Hepatitis B virus.

OS Key Location/Qualifiers

XX Region 1..65

FT /label= PreS2_region

FT 66..281

FT /note= "This region corresponds to the S protein (AAM52694)"

XX US6306625-B1.

XX 23-OCT-2001.

XX 25-MAR-1997; 97US-008233578.

XX 30-DEC-1988; 88US-00292202.

PR 19-JUN-1989; 89US-00368401.

PR 28-FEB-1992; 92US-00846487.

PR 08-MAR-1993; 93US-00028037.

PR 21-DEC-1993; 93US-00170610.

PR 26-OCT-1994; 94US-00329354.

PR 05-JUL-1995; 95US-00498545.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Jacobs E, Rutgers A;

DR WPI; 2002-048341/06.
 DR N-PSDB; ABA02358.
 XX Producing a hepatitis B surface antigen (HBsAg) particle, useful for
 PT obtaining expression of mixed HBsAg particle for use as vaccine
 PT components, comprises co-expressing the S antigen of HBsAg and another
 PT protein as fusion proteins in yeast.
 XX Claim 4; Col 5-8; 16pp; English.
 PS
 XX The invention relates to a method of producing a hepatitis B virus (HBV)
 CC surface antigen (HBsAg) particle of mixed polypeptide composition in
 CC yeast cells, especially Saccharomyces cerevisiae. The method comprises
 CC the coexpression of the gene encoding the HBV major surface protein (S
 CC protein) and a gene encoding the S protein plus at least a portion of the
 CC HBV preS12 polypeptide, optionally fused to another polypeptide (e.g., a
 CC protein from a pathogenic microorganism, virus or cell, or an epitope
 CC thereof). Particularly preferred polypeptides for expression in the
 CC fusion protein are a Plasmodium circumsporozoite protein or epitopes
 CC thereof, the HIV (human immunodeficiency virus) envelope proteins gp120
 CC and gp160 or epitopes thereof, proteins derived from the influenza virus
 CC haemagglutinin HAZ subunit, or epitopes of the HBV core antigen. The
 CC invention also encompasses the coexpression of a third protein comprising
 CC all or a portion of the HBV preS12 polypeptide, optionally fused to an
 CC immunogenic polypeptide such as those listed above, with the proviso that
 CC the two preS12 polypeptide components expressed in the yeast cell are
 CC not identical. The HBsAg particles obtained by the method are of mixed
 CC composition, i.e., a multimeric assembly of the S protein and one or two
 CC preS12 or hybrid proteins. Such particles can therefore carry different
 CC heterologous epitopes which make them useful as vaccine components. The
 CC present sequence represents the M (middle) HBsAg protein, which may be a
 CC component of the mixed composition HBsAg of the invention
 XX Sequence 281 AA;

Query Match 92.7%; Score 1187; DB 5; Length 281;
 Best Local Similarity 92.1%; Pred. No. 7e-102;
 Matches 209; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 QY 1 NMENIASGLGLPLVLQAGFFLLTKILTIPOSLSWNTSLNPLGSPVCLGQNSQSQISS 60
 DB 55 NMENITSGFLGPLVLQAGFFLLTKILTIPOSLSWNTSLNPLGSPVCLGQNSQSPTSN 114
 QY 61 HSPTCCTPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPCLIPGTTTSTG 120
 DB 115 HSPTSCTPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPCLIPGTTTSTG 174
 QY 121 PKCTCTTPAQTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLILVFP 180
 DB 175 PKCTCTTPAQTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLILVFP 234
 QY 181 VQWFVGLSPTVWLSVIWMWFWGSPSLYNILSPFMPPLPIFFCLWYI 227
 DB 235 VQWFVGLSPTVWLSAIWMMWYWGSPSLYSIVSPFIPPLPIFFCLWYI 281

RESULT 8
 AAR10852
 ID AAR10852 standard; protein; 387 AA.
 XX
 AC AAR10852;
 XX
 XX 25-MAR-2003 (revised)
 DT 29-APR-1991 (first entry)
 XX
 DE Modified hepatitis B virus large protein (II).
 XX
 KW Hepatitis B virus; large surface protein; L protein;
 KW N-glycosylation site; vaccines.
 XX
 OS Hepatitis B virus.
 XX
 FH Key Location/Qualifiers

Region 1. .108
 /label= pre-S1
 Region 109. .160
 /label= pre-S2
 Region 161. .387
 /label= S-region
 XX EP414374-A.
 XX
 XX 27-FEB-1991.
 XX
 XX 19-JUL-1990; 90BP-00307900.
 XX
 XX 25-JUL-1989; 89US-00385342.
 PR 03-AUG-1989; 89US-00389184.
 XX
 XX (SMIK) SMITHKLINE BIOLOGIC.
 PA (COMB/) COMBERBACH M.
 XX
 XX Comberbach M, Harford N, Cabezon T, Rutgers A, Voet P, Jacobs E;
 PI Hollenberg CP, Janowicz ZA, Merckelbach AJ;
 DR WPI; 1991-059585/09.
 DR N-PSDB; AAQ10679.
 XX
 XX Modified hepatitis B virus large surface protein - has amino acid
 PT sequence encoding L protein used in vaccine for treating or preventing
 PT hepatitis B without side-effects.
 XX
 PS Disclosure; Page 4-7; 79pp; English.
 XX
 CC The modified L protein has the N-glycosylation site NST (amino acid 123-
 CC 125) of the wild-type sequence deleted. The amino acids may opt. be
 CC replaced with other amino acids. (The first eleven amino acids of the ad
 CC sequence are not given). The modified product may be used alone or in a
 CC composite particle comprising at least two polypeptides corresp. to all
 CC or part of a protein having the biological activity of one of the
 CC hepatitis B surface antigens. The composite particles are useful for
 CC preparing improved hepatitis B vaccines or for treating of HBV. See also
 CC AAQ10677/79. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25
 CC -MAR-2003 to correct PI field.)
 XX
 SQ Sequence 387 AA;

Query Match 92.7%; Score 1187; DB 2; Length 387;
 Best Local Similarity 92.1%; Pred. No. 9.8e-102;
 Matches 209; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 QY 1 NMENIASGLGLPLVLQAGFFLLTKILTIPOSLSWNTSLNPLGSPVCLGQNSQSQISS 60
 DB 160 NMENITSGFLGPLVLQAGFFLLTKILTIPOSLSWNTSLNPLGSPVCLGQNSQSPTSN 219
 QY 61 HSPTCCTPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPCLIPGTTTSTG 120
 DB 220 HSPTSCTPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPCLIPGTTTSTG 279
 QY 121 PKCTCTTPAQTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLILVFP 180
 DB 280 PKCTCTTPAQTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLILVFP 339
 QY 181 VQWFVGLSPTVWLSVIWMWFWGSPSLYNILSPFMPPLPIFFCLWYI 227
 DB 340 VQWFVGLSPTVWLSAIWMMWYWGSPSLYSIVSPFIPPLPIFFCLWYI 386

RESULT 9
 AAR10851
 ID AAR10851 standard; protein; 388 AA.
 XX
 AC AAR10851;
 XX
 XX 25-MAR-2003 (revised)
 DT 29-APR-1991 (first entry)

XX Modified hepatitis B virus large protein (I).

XX Hepatitis B virus; large surface protein; L protein; myristylation;

XX vaccines.

XX Hepatitis B virus.

XX Key Location/Qualifiers

XX Region 1..107

XX /label= pre-S1

XX Region 108..162

XX /label= pre-S2

XX Region 163..388

XX /label= S-region

XX EP414374-A.

XX

XX 27-FEB-1991.

XX

XX 19-JUL-1990; 90EP-00307900.

XX

XX 25-JUL-1989; 89US-00385342.

XX

XX 03-AUG-1989; 89US-00389184.

XX

XX (SMK) SMITHKLINE BIOLOGIC.

XX (COMB/) COMBERBACH M.

XX

XX Comberbach M, Harford N, Cabezon T, Rutgers A, Voet P, Jacobs E;

XX Hollenberg CP, Janowicz ZA, Merckelbach AJ;

XX

XX WPI: 1991-059585/09.

XX

XX N-PSDB; AAQ10678.

XX

XX Modified hepatitis B virus large surface protein - has amino acid

XX sequence encoding L protein used in vaccine for treating or preventing

XX hepatitis B without side-effects.

XX

XX Disclosure; Page 4-7; 79pp; English.

XX

XX The modified L protein has the Gly 13 amino acid in the preS1 region of

XX the wild-type sequence deleted. The deletion results in the synthesis of

XX a non-myristylated L protein. (The first amino of the ad sequence are not

XX given). The modified product may be used alone or in a composite particle

XX comprising at least two polypeptides corresp. to all or part of a protein

XX having the biological activity of one of the hepatitis B surface

XX antigens. The composite particles are useful for preparing improved

XX hepatitis B vaccines or for treating of HBV. See also AAQ10677-79.

XX (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to

XX correct PI field.)

XX

XX Sequence 388 AA;

SQ

Query Match 92.7%; Score 1187; DB 2; Length 388;

Best Local Similarity 92.1%; Pred. No. 9.8e-102;

Matches 209; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 NNEINISGFLGFLVQLQAGFLLRLTIPQSLDSWMTSLNFLGSPVCLGQNSQSPSTN 221

Db 162 NNEINISGFLGFLVQLQAGFLLRLTIPQSLDSWMTSLNFLGSPVCLGQNSQSPSTN 221

QY 61 HSPCCPFCGGRWMLRRRIIFLCILLCLIFLLVLLDYQGLMFPVCPPIPGSTTTSTG 120

Db 222 HSPCCPFCGGRWMLRRRIIFLCILLCLIFLLVLLDYQGLMFPVCPPIPGSTTTNTG 281

QY 121 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPISWAFAXYLWENASVRFSLSLVVPF 180

Db 282 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPISWAFAXYLWENASVRFSLSLVVPF 341

QY 181 VQWFGVLSPTVWLSVWMMWFGVLSNLSLSPFLLPIPFCLWVYI 227

Db 342 VQWFGVLSPTVWLSVWMMWFGVLSNLSLSPFLLPIPFCLWVYI 388

RESULT 10

AAM52682

ID AAM52682 standard; protein; 389 AA.

XX

XX AAM52682;

XX

XX 26-FEB-2002 (first entry)

XX

XX Hepatitis B virus surface antigen L protein.

XX

XX HBV; S protein; major surface protein; M protein; L protein;

XX surface antigen; HBsAg; yeast; coexpression; preS1S2 polypeptide;

XX fusion protein; epitope; antiviral; antiparasitic; vaccine;

XX mixed composition.

XX

XX Hepatitis B virus.

XX

XX Key Location/Qualifiers

XX Region 1..163

XX /label= PreS1S2_region

XX /note= "This region corresponds to the preS1S2

XX polypeptide (AAM52695)"

XX Region 1..108

XX /label= PreS1_region

XX Region 109..389

XX /note= "This region corresponds to the M protein

XX (AAM52693)"

XX Region 109..163

XX /label= PreS2_region

XX Region 164..389

XX /note= "This region corresponds to the S protein

XX (AAM52694)"

XX

XX US6306625-B1.

XX

XX 23-OCT-2001.

XX

XX 25-MAR-1997; 97US-00823578.

XX

XX 30-DEC-1988; 88US-00292202.

XX

XX 19-JUN-1989; 89US-00388401.

XX

XX 28-FEB-1992; 92US-00846487.

XX

XX 08-MAR-1993; 93US-00028037.

XX

XX 21-DEC-1993; 93US-00170610.

XX

XX 26-OCT-1994; 94US-00329354.

XX

XX 05-JUL-1995; 95US-00498545.

XX

XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.

XX

XX Jacobs E, Rutgers A;

XX

XX WPI: 2002-048341/06.

XX

XX N-PSDB; AAB02358.

XX

XX Producing a hepatitis B surface antigen (HBsAg) particle, useful for

XX obtaining expression of mixed HBsAg particle for use as vaccine

XX components, comprises co-expressing the S antigen of HBsAg and another

XX protein as fusion proteins in yeast.

XX

XX Claim 5; Col 3-8; 16pp; English.

XX

XX The invention relates to a method of producing a hepatitis B virus (HBV)

XX surface antigen (HBsAg) particle of mixed polypeptide composition in

XX yeast cells, especially Saccharomyces cerevisiae. The method comprises

XX the coexpression of the gene encoding the HBV major surface protein (S

XX protein) and a gene encoding the S protein plus at least a portion of the

XX HBV preS1S2 polypeptide, optionally fused to another polypeptide (e.g., a

XX protein from a pathogenic microorganism, virus or cell, or an epitope

XX thereof). Particularly preferred polypeptides for expression in the

XX fusion protein are a Plasmodium circumsporozoite protein or epitopes

XX thereof, the HIV (human immunodeficiency virus) envelope proteins gp120

XX and gp160 or epitopes thereof, proteins derived from the influenza virus

CC haemagglutinin HA2 subunit, or epitopes of the HBV core antigen. The
CC invention also encompasses the coexpression of a third protein comprising
CC all or a portion of the HBV preS2 polypeptide, optionally fused to an
CC immunogenic polypeptide such as those listed above, with the proviso that
CC the two preS2 polypeptide components expressed in the yeast cell are
CC not identical. The HBsAg particles obtained by the method are of mixed
CC composition, i.e., a multimeric assembly of the S protein and one or two
CC preS1S2 or hybrid proteins. Such particles can therefore carry different
CC heterologous epitopes which make them useful as vaccine components. The
CC present sequence represents the L (large) HBsAg protein, which may be a
CC component of the mixed composition HBsAg of the invention
XX
SQ Sequence 389 AA;

Query Match 92.7%; Score 1187; DB 5; Length 389;
Best Local Similarity 92.1%; Pred. No. 9.8e-102; Indels 0; Gaps 0;
Matches 209; Conservative 7; Mismatches 11;
QY 1 NMENIASGLLGLPVLVLAQGFLLTKLTIPQSLDSWMTSLNLFGLGTPVCLGNSQSQSISS 60
DB 163 NMENITSGFLPVLVLAQGFLLTKLTIPQSLDSWMTSLNLFGLGTPVCLGNSQSPTSN 222
QY 61 HSPTCCPPICPGYRWMLRRRIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
DB 223 HSPTSCPPICPGYRWMLRRRIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTNTG 282
QY 121 PKCTCTTPAQGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWEMASVRFSLVLPVF 180
DB 293 PKCTCTTPAQGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWEMASVRFSLVLPVF 342
QY 181 VQMFVGLSPTVWLSVIMWMMWFGPSLYNLTSPFPLPIFFCLWYI 227
DB 343 VQMFVGLSPTVWLSAIIWMMWFGPSLYNLTSPFPLPIFFCLWYI 389

RESULT 11

AAR37797
ID AAR37797 standard; protein; 424 AA.

XX AC AAR37797;

XX 25-MAR-2003 (revised)

XX 27-SEP-1993 (first entry)

XX RTS* protein.

XX RTS; expression cassette; hybrid protein; S. cerevisiae; TDH3; cloning;
XX circumporozoite protein; CSP; Plasmodium falciparum; strain 7G8;
XX hepatitis B virus; HBV; adw serotype; preS2 protein; S protein.

XX Synthetic.

XX Key Location/Qualifiers

XX Region 1 /note= "Derived from S. cerevisiae TDH3 gene sequence"

XX Region 2, 4

XX Protein /note= "Cloning artefact"

XX /note= "Represents amino acids 210-398 of the CSP of P.
XX falciparum"

XX Region 194, .197

XX /note= "Carboxy terminal amino acids from HBV (adw
XX serotype) preS2 protein"

XX Protein 198, .424

XX /note= "S protein of HBV (adw serotype)"

XX WO9310152-A1.

XX 27-MAY-1993.

XX 11-NOV-1992; 92WO-EP002591.

XX 16-NOV-1991; 91GB-00024390.

PR 27-FEB-1992; 92US-00842694.
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX De Wilde M, Cohen J;

XX WPI; 1993-182494/22.

XX N-PSDB; AAQ42567.

XX Hybrid protein comprising Plasmodium circumporozoite protein and HBsAg -
XX useful as a vaccine for treating patients susceptible to Plasmodium
XX infections.

XX Disclosure; Fig 9; 59pp; English.

XX This sequence represents the RTS* hybrid protein which is encoded by the
XX RTS* expression cassette. This hybrid consists of a methionine residue
XX derived from S. cerevisiae TDH3 gene sequence, three amino acids, Met-Ala
XX -Pro, derived from a nucleotide sequence created by the cloning procedure
XX used to construct the hybrid gene, a stretch of 189 amino acids
XX representing amino acids 210 to 398 of the circumporozoite protein (CSP)
XX of Plasmodium falciparum strain NF54, an amino acid Arg created by the
XX cloning procedure, four amino acids, Pro-Val-Thr-Asn, representing the
XX four carboxy terminal residues of hepatitis B virus (HBV), adw serotype,
XX preS2 protein, and a stretch of 226 amino acids specifying the S protein
XX of HBV, adw serotype. This protein, and RTS (see also AAR37796), may be
XX combined with an adjuvant and used in a vaccine for preventing plasmodium
XX infections. The vaccines produce a humoral response and also a cellular
XX immune response. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 424 AA;

Query Match 92.7%; Score 1187; DB 2; Length 424;

Best Local Similarity 92.1%; Pred. No. 1.1e-101;

Matches 209; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 NMENIASGLLGLPVLVLAQGFLLTKLTIPQSLDSWMTSLNLFGLGTPVCLGNSQSQSISS 60

DB 198 NMENITSGFLPVLVLAQGFLLTKLTIPQSLDSWMTSLNLFGLGTPVCLGNSQSPTSN 257

QY 61 HSPTCCPPICPGYRWMLRRRIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120

DB 258 HSPTSCPPICPGYRWMLRRRIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTNTG 317

QY 121 PKCTCTTPAQGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWEMASVRFSLVLPVF 180

DB 318 PKCTCTTPAQGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWEMASVRFSLVLPVF 377

QY 181 VQMFVGLSPTVWLSVIMWMMWFGPSLYNLTSPFPLPIFFCLWYI 227

DB 378 VQMFVGLSPTVWLSAIIWMMWFGPSLYNLTSPFPLPIFFCLWYI 424

RESULT 12

AAR37796

ID AAR37796 standard; protein; 424 AA.

XX AC AAR37796;

XX 25-MAR-2003 (revised)

XX 27-SEP-1993 (first entry)

XX RTS protein.

XX RTS; expression cassette; hybrid protein; S. cerevisiae; TDH3; cloning;
XX circumporozoite protein; CSP; Plasmodium falciparum; strain 7G8;
XX hepatitis B virus; HBV; adw serotype; preS2 protein; S protein.

XX Synthetic.

XX Key Location/Qualifiers

XX Region 1

XX /note= "Derived from S. cerevisiae TDH3 gene sequence"

FT Region 2. 4
 FT /note= "Cloning artefact"
 FT Protein 5.193
 FT /note= "Represents amino acids 210-398 of the CSP of P.
 FT falciparum"
 FT Region 194.197
 FT /note= "Carboxy terminal amino acids from HBV (adv
 FT serotype) pres2 protein"
 FT Protein 198.424
 FT /note= "S protein of HBV (adv serotype)"
 XX
 PN WO9310152-A1.
 XX
 XX 27-MAY-1993.
 XX
 XX 11-NOV-1992; 92WO-EP002591.
 XX
 PR 16-NOV-1991; 91GB-00024390.
 PR 27-FEB-1992; 92US-00842694.
 XX
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI De Wilde M, Cohen J;
 XX
 XX WPI; 1993-182494/22.
 DR N-PSDB; AAQ42566.
 XX
 XX Hybrid protein comprising Plasmodium circumsporozoite protein and HBeAg -
 PT useful as a vaccine for treating patients susceptible to Plasmodium
 PT infections.
 XX
 XX Disclosure; Fig 5; 59pp; English.
 PS
 XX This sequence represents the RTS hybrid protein which is encoded by the
 CC RTS expression cassette. This hybrid consists of a methionine residue
 CC derived from S. cerevisiae TDH3 gene sequence, three amino acids, Met-Ala
 CC -Pro, derived from a nucleotide sequence created by the cloning procedure
 CC used to construct the hybrid gene, a stretch of 189 amino acids
 CC representing amino acids 210 to 398 of the circumsporozoite protein (CSP)
 CC of Plasmodium falciparum strain 7G8, an amino acid Arg created by the
 CC cloning procedure, four amino acids, Pro-Val-Thr-Asn, representing the
 CC four carboxy terminal residues of hepatitis B virus (HBV), adv serotype,
 CC pres2 protein, and a stretch of 226 amino acids specifying the S protein
 CC of HBV, adv serotype. This protein, and RTS* (see also AAR47797), may be
 CC combined with an adjuvant and used in a vaccine for preventing plasmodium
 CC infections. The vaccines produce a humoral response and also a cellular
 CC immune response. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 424 AA;
 Query Match 92.7%; Score 1187; DB 2; Length 424;
 Best Local Similarity 92.1%; Pred. No. 1.1e-101;
 Matches 209; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 QY 1 NMENIASGLGLPLVLQAGFFLLTKILTIPOSLSWSMTSLNFIQGGPTVCLGQNSQSQISS 60
 DB 198 NMENITSGFLGLPLVLQAGFFLLTKILTIPOSLSWSMTSLNFIQGGPTVCLGQNSQSPTS 257
 QY 61 HSPTCCPPICGYRWMLRRRIIFELCLLCLIFLLVLDYQGMPLPVCPLIPGTTTSTG 120
 DB 258 HSPTSCPPICGGRWMLRRRIIFELCLLCLIFLLVLDYQGMPLPVCPLIPGTTTNTG 317
 QY 121 PKCTCTTTPAQGTSMPFSCCTCKPTDRNCTCIPIPSWAFKYLWNASVRFSLWLLVPP 180
 DB 318 PKCTCTTTPAQGNSMFPSCCTCKPTDRNCTCIPIPSWAFKYLWNASVRFSLWLLVPP 377
 QY 181 VQWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPNPLPIPFCLWYI 227
 DB 378 VQWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPNPLPIPFCLWYI 424
 RESULT 13
 AAG66928

ID AAG66928 standard; protein; 400 AA.
 XX
 AC AAG66928;
 XX
 DT 19-OCT-2001 (first entry)
 XX
 DE HBV genotype A pres1/pres2/HBsAg polypeptide.
 XX
 KW Hepatitis B virus; HBV; preCore; Core; pres1; pres2; HBS; HBx; HBp01;
 KW HBSAg; antiviral; vaccine; genotype G; genotyping; HbsAg; HBeAg.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200140279-A2.
 PD 07-JUN-2001.
 XX
 XX 20-NOV-2000; 2000WO-EP011526.
 XX
 PR 03-DEC-1999; 99EP-00870252.
 PR 07-DEC-1999; 99US-0169287P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 XX Stuyver L, Van Geyt C, De Gendt S;
 PI WPI; 2001-374785/39.
 DR
 XX
 XX Novel isolated and/or purified hepatitis B virus polypeptide and
 PT polynucleotide sequences that are phylogenetically different from HBV
 PT genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
 PT therapy.
 XX
 XX Example 3; Fig 6; 94pp; English.
 PS
 XX The invention relates to the complete nucleic acid sequence of a new
 CC human hepatitis B virus (HBV) genotype, provisionally named genotype G.
 CC This genotype was found with a high prevalence in patients chronically
 CC infected with HBV and residing in Europe and the USA. The invention
 CC relates to a fully defined sequence of 3248 nucleotides as given in
 CC specification, a sequence with 92% identity to the given sequence, or
 CC sequence that is degenerate to the mentioned sequences. These
 CC polynucleotides are useful for HBV genotyping. The proteins encoded by
 CC the polynucleotides are useful for detecting antibodies in a biological
 CC sample. Ligands that bind to the proteins and antibodies directed against
 CC the proteins are useful for detecting the proteins and for detecting
 CC HBsAg and HBeAg (precursor proteins). They are also useful for
 CC preparing a vaccine or medicament for treating HBV infections. The
 CC present sequence is provided in an amino acid sequence alignment of the
 CC pres1, pres2 and HBeAg open reading frame of the different HBV genotypes
 XX
 SQ Sequence 400 AA;
 Query Match 92.5%; Score 1185; DB 4; Length 400;
 Best Local Similarity 92.1%; Pred. No. 1.6e-101;
 Matches 209; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
 QY 1 NMENIASGLGLPLVLQAGFFLLTKILTIPOSLSWSMTSLNFIQGGPTVCLGQNSQSQISS 60
 DB 174 NMENITSGFLGLPLVLQAGFFLLTKILTIPOSLSWSMTSLNFIQGGPTVCLGQNSQSPTS 233
 QY 61 HSPTCCPPICGYRWMLRRRIIFELCLLCLIFLLVLDYQGMPLPVCPLIPGTTTSTG 120
 DB 234 HSPTSCPPICGGRWMLRRRIIFELCLLCLIFLLVLDYQGMPLPVCPLIPGTTTSTG 293
 QY 121 PKCTCTTTPAQGTSMPFSCCTCKPTDRNCTCIPIPSWAFKYLWNASVRFSLWLLVPP 180
 DB 294 PKCTCTTTPAQGNSMFPSCCTCKPTDRNCTCIPIPSWAFKYLWNASVRFSLWLLVPP 353
 QY 181 VQWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPNPLPIPFCLWYI 227
 DB 354 VQWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPNPLPIPFCLWYI 400

Mon Jul 26 11:38:44 2004

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Page 10

Search completed: July 26, 2004, 11:27:11
Job time : 90.076 secs

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OM protein - protein search, using sw model

Run on: July 26, 2004, 11:25:30 ; Search time 26.332 Seconds
(without alignments)
445.051 Million cell updates/sec

Title: US-09-719-533A-3_COPY_174_400

Sequence: 1 NMENIASGLLGPLLVLQGF.....NILSPFWPLLPFFCLWVYI 227

Scoring table: BLOSUM62

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1213	94.7	228	1 US-08-447-591-2	Sequence 2, Appli
2	1213	94.7	228	1 US-08-450-943-2	Sequence 2, Appli
3	1213	94.7	228	1 US-08-059-031-2	Sequence 2, Appli
4	1213	94.7	228	5 US-08-450-942-2	Sequence 2, Appli
5	1213	94.7	228	5 PCT-US94-05090-2	Sequence 3, Appli
6	1194	93.2	228	1 US-08-447-591-3	Sequence 3, Appli
7	1194	93.2	228	1 US-08-450-943-3	Sequence 3, Appli
8	1194	93.2	228	1 US-08-059-031-3	Sequence 3, Appli
9	1194	93.2	228	2 US-08-450-942-3	Sequence 3, Appli
10	1194	93.2	228	5 PCT-US94-05090-3	Sequence 3, Appli
11	1187	92.7	423	2 US-08-760-797A-1	Sequence 1, Appli
12	1187	92.7	424	2 US-08-760-797A-1	Sequence 3, Appli
13	1187	92.7	424	3 US-08-932-929B-1	Sequence 1, Appli
14	1187	92.7	424	3 US-08-932-929B-3	Sequence 3, Appli
15	1184	92.4	226	6 5196194-21	Patent No. 5196194
16	1184	92.4	226	6 5436139-5	Patent No. 5436139
17	1179	92.0	225	6 5436139-4	Patent No. 5436139
18	1166	91.0	237	1 US-08-378-011A-1	Sequence 1, Appli
19	1166	91.0	276	6 5164485-2	Patent No. 5164485
20	1164.5	90.9	395	6 5196194-18	Patent No. 5196194
21	1164	90.9	226	6 5198348-1	Patent No. 5198348
22	1164	90.9	281	1 US-08-105-483-214	Sequence 214, App
23	1164	90.9	281	1 US-08-709-209-214	Sequence 214, App
24	1164	90.9	281	1 US-08-458-101-214	Sequence 12, Appl
25	1164	90.9	281	4 US-09-247-890-12	Sequence 12, Appl
26	1164	90.9	281	4 US-09-724-969-12	Sequence 12, Appl
27	1164	90.9	281	4 US-09-724-852-12	Sequence 12, Appl

28 1164 90.9 389 1 US-08-105-483-216 Sequence 216, App
29 1164 90.9 389 1 US-08-105-483-219 Sequence 219, App
30 1164 90.9 389 1 US-08-709-209-216 Sequence 216, App
31 1164 90.9 389 1 US-08-709-209-219 Sequence 219, App
32 1164 90.9 389 1 US-08-458-101-216 Sequence 216, App
33 1164 90.9 389 1 US-08-458-101-219 Sequence 219, App
34 1164 90.9 389 3 US-08-486-099-106 Sequence 106, App
35 1164 90.9 389 3 US-08-360-107A-116 Sequence 116, App
36 1164 90.9 389 3 US-08-484-223B-106 Sequence 106, App
37 1164 90.9 389 3 US-08-919-597-106 Sequence 106, App
38 1164 90.9 389 3 US-08-475-668A-106 Sequence 106, App
39 1164 90.9 389 3 US-08-485-551A-106 Sequence 106, App
40 1164 90.9 389 3 US-08-471-913A-106 Sequence 106, App
41 1164 90.9 389 3 US-08-485-264A-106 Sequence 106, App
42 1164 90.9 389 4 US-08-474-349A-106 Sequence 106, App
43 1164 90.9 389 4 US-08-470-896-106 Sequence 106, App
44 1164 90.9 389 4 US-08-485-546A-106 Sequence 106, App
45 1161 90.6 228 1 US-08-447-591-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-447-591-2
; Sequence 2, Application US/08447591
; Patent No. 5591440
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MINMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,591
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,031
; FILING DATE: 07-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-447-591-2

Query Match 94.7%; Score 1213; DB 1; Length 228;
Best Local Similarity 94.3%; Pred. No. 2.6e-108;
Matches 215; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

QY 2 MENIASGLLGLLVLAQGFLLTKLTIPQSLDSWWTSLNLFGLGPTVCLGQNSQSISSH 61
DB 1 MENTTSGLLGLLVLAQGFLLTKLTIPQSLDSWWTSLNLFGLGPTVCSGQNSQSISSH 60
QY 62 SPTCCPPICPGYRWMCLRRFIFLCILLCLIFLLVLLDYQGLMPVCPPLIPGSGSTTSTGP 121
DB 61 SPTCCPPICPGYRWMCLRRFIFLCILLCLIFLLVLLDYQGLMPVCPPLIPGSGSTTSTGP 120
QY 122 CK--TCTTTPAGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLLVP 179
DB 121 CRNTTCTTTPAGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLLVP 180
QY 180 FVQWFGVLSPTVWLSVIMMMFWGSPSLYNILSPFMPLLPIFFCLWVYI 227
DB 181 FVQWFGVLSPTVWLSVIMMMFWGSPSLYNILSPFMPLLPIFFCLWVYI 228

RESULT 2

US-08-450-943-2
; Sequence 2, Application US/08450943
; Patent No. 5593825
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLIS, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,943
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-943-2

Query Match 94.7%; Score 1213; DB 1; Length 228;
Best Local Similarity 94.3%; Pred. No. 2.6e-108;
Matches 215; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

QY 2 MENIASGLLGLLVLAQGFLLTKLTIPQSLDSWWTSLNLFGLGPTVCLGQNSQSISSH 61
DB 1 MENTTSGLLGLLVLAQGFLLTKLTIPQSLDSWWTSLNLFGLGPTVCSGQNSQSISSH 60
QY 62 SPTCCPPICPGYRWMCLRRFIFLCILLCLIFLLVLLDYQGLMPVCPPLIPGSGSTTSTGP 121

DB 61 SPTCCPPICPGYRWMCLRRFIFLCILLCLIFLLVLLDYQGLMPVCPPLIPGSGSTTSTGP 120
QY 122 CK--TCTTTPAGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLLVP 179
DB 121 CRNTTCTTTPAGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLLVP 180
QY 180 FVQWFGVLSPTVWLSVIMMMFWGSPSLYNILSPFMPLLPIFFCLWVYI 227
DB 181 FVQWFGVLSPTVWLSVIMMMFWGSPSLYNILSPFMPLLPIFFCLWVYI 228

RESULT 3

US-08-059-031-2
; Sequence 2, Application US/08059031
; Patent No. 5595739
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/059,031
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-059-031-2

Query Match 94.7%; Score 1213; DB 1; Length 228;
Best Local Similarity 94.3%; Pred. No. 2.6e-108;
Matches 215; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

QY 2 MENIASGLLGLLVLAQGFLLTKLTIPQSLDSWWTSLNLFGLGPTVCLGQNSQSISSH 61
DB 1 MENTTSGLLGLLVLAQGFLLTKLTIPQSLDSWWTSLNLFGLGPTVCSGQNSQSISSH 60
QY 62 SPTCCPPICPGYRWMCLRRFIFLCILLCLIFLLVLLDYQGLMPVCPPLIPGSGSTTSTGP 121
DB 61 SPTCCPPICPGYRWMCLRRFIFLCILLCLIFLLVLLDYQGLMPVCPPLIPGSGSTTSTGP 120
QY 122 CK--TCTTTPAGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLLVP 179
DB 121 CRNTTCTTTPAGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLLVP 180
QY 180 FVQWFGVLSPTVWLSVIMMMFWGSPSLYNILSPFMPLLPIFFCLWVYI 227

Db 181 FVQWFGVLSPTVWLSVIMWYWGPSLYNLSLSPFMPLLPIFYCLWYI 228

RESULT 4

US-08-450-942-2

; Sequence 2, Application US/08450942

; Patent No. 5925512

; GENERAL INFORMATION:

; APPLICANT: CARMAN, WILLIAM

; APPLICANT: DECKER, RICHARD H

; APPLICANT: WALLACE, LESLEY

; APPLICANT: MIMMS, LARRY T

; APPLICANT: SOLOMON, LARRY R

; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

; STREET: ONE ABBOTT PARK ROAD

; CITY: ABBOTT PARK

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,942

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: FOREMSKI, PRISCILLA E.

; REGISTRATION NUMBER: 33,207

; REFERENCE/DOCKET NUMBER: 5347.US.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-6365

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 228 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-450-942-2

Query Match 94.7%; Score 1213; DB 2; Length 228;

Best Local Similarity 94.3%; Pred. No. 2.6e-108;

Matches 215; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

Qy 2 MENIASGLGLPVLVLAQGFLLTKLTIPQSLDSWNTSLNPLGPTVCLQNSQSQISSH 61

Db 1 MENTTSGLLGPLLVLAQGFLLTKLTIPQSLDSWNTSLNPLGPTVCLQNSQSQISSH 60

Qy 62 SPTCCPPICPGYRWMLRRFIFLCILLCLIFLLVLDYQGMPLVCPPLPGSTTTSTGP 121

Db 61 SPTCCPPICPGYRWMLRRFIFLCILLCLIFLLVLDYQGMPLVCPPLPGSTTTSTGP 120

Qy 122 CK--TCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFSLSLVLP 179

Db 121 CRNTTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFSLSLVLP 180

Qy 180 FVQWFGVLSPTVWLSVIMWYWGPSLYNLSLSPFMPLLPIFYCLWYI 227

Db 181 FVQWFGVLSPTVWLSVIMWYWGPSLYNLSLSPFMPLLPIFYCLWYI 228

RESULT 5

PCT-US94-05090-2

; Sequence 2, Application PC/TUS9405090

; GENERAL INFORMATION:

; APPLICANT: CARMAN, WILLIAM

; APPLICANT: DECKER, RICHARD H

; APPLICANT: WALLACE, LESLEY

; APPLICANT: MIMMS, LARRY T

; APPLICANT: SOLOMON, LARRY R

; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

; STREET: ONE ABBOTT PARK ROAD

; CITY: ABBOTT PARK

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/05090

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: FOREMSKI, PRISCILLA E.

; REGISTRATION NUMBER: 33,207

; REFERENCE/DOCKET NUMBER: 5347.US.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 708-937-6365

; TELEFAX: 708-938-2623

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 228 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US94-05090-2

Query Match 94.7%; Score 1213; DB 5; Length 228;

Best Local Similarity 94.3%; Pred. No. 2.6e-108;

Matches 215; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

Qy 2 MENIASGLGLPVLVLAQGFLLTKLTIPQSLDSWNTSLNPLGPTVCLQNSQSQISSH 61

Db 1 MENTTSGLLGPLLVLAQGFLLTKLTIPQSLDSWNTSLNPLGPTVCLQNSQSQISSH 60

Qy 62 SPTCCPPICPGYRWMLRRFIFLCILLCLIFLLVLDYQGMPLVCPPLPGSTTTSTGP 121

Db 61 SPTCCPPICPGYRWMLRRFIFLCILLCLIFLLVLDYQGMPLVCPPLPGSTTTSTGP 120

Qy 122 CK--TCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFSLSLVLP 179

Db 121 CRNTTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFSLSLVLP 180

Qy 180 FVQWFGVLSPTVWLSVIMWYWGPSLYNLSLSPFMPLLPIFYCLWYI 227

Db 181 FVQWFGVLSPTVWLSVIMWYWGPSLYNLSLSPFMPLLPIFYCLWYI 228

RESULT 6

US-08-447-591-3

; Sequence 3, Application US/08447591

; Patent No. 5591440

; GENERAL INFORMATION:

; APPLICANT: CARMAN, WILLIAM

; APPLICANT: DECKER, RICHARD H

; APPLICANT: WALLACE, LESLEY

; APPLICANT: MIMMS, LARRY T

; APPLICANT: SOLOMON, LARRY R

; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

```

; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/447,591
; APPLICATION NUMBER: 07-MAY-1993
; PRIORITY INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-447-591-3

Query Match 93.2%; Score 1194; DB 1; Length 228;
Best Local Similarity 92.1%; Pred. No. 1.7e-106;
Matches 210; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 2 MENIASGLGLPVLVQAGFFLLTKILTIPOSLSWNTSLNPLGPTVCLGQNSQSOISSH 61
DB 1 MENTTSGLLGLPVLVQAGFFLLTKILTIPOSLSWNTSLNPLGPTVCLGQNSQSOISSH 60
QY 62 SPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGLMPVCLIPGSTTTSTGP 121
DB 61 SPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGLMPVCLIPGSTTTSTGP 120
QY 122 CK--TCTTPAQGTSMFPSCCCTKPTDRNCTCIPIPSSWAFKYLWNASVRFWSLSLVP 179
DB 121 CRNTTCTTTPAQGTSMFPSCCCTKPTDRNCTCIPIPSSWAFKYLWNASVRFWSLSLVP 180
QY 180 FVQWVGLSPTVWLSVIMMWGFSLYNLSLSPMPLLPFFCLWVYI 227
DB 181 IVQWVAGLSPTVWLSVIMMWGFSLYNLSLSPMPLLPFFCLWVYI 228

RESULT 8
US-08-059-031-3
; Sequence 3, Application US/08059031
; Patent No. 5595739
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/059,031

; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/447,591
; APPLICATION NUMBER: 07-MAY-1993
; PRIORITY INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-447-591-3

Query Match 93.2%; Score 1194; DB 1; Length 228;
Best Local Similarity 92.1%; Pred. No. 1.7e-106;
Matches 210; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 2 MENIASGLGLPVLVQAGFFLLTKILTIPOSLSWNTSLNPLGPTVCLGQNSQSOISSH 61
DB 1 MENTTSGLLGLPVLVQAGFFLLTKILTIPOSLSWNTSLNPLGPTVCLGQNSQSOISSH 60
QY 62 SPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGLMPVCLIPGSTTTSTGP 121
DB 61 SPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGLMPVCLIPGSTTTSTGP 120
QY 122 CK--TCTTPAQGTSMFPSCCCTKPTDRNCTCIPIPSSWAFKYLWNASVRFWSLSLVP 179
DB 121 CRNTTCTTTPAQGTSMFPSCCCTKPTDRNCTCIPIPSSWAFKYLWNASVRFWSLSLVP 180
QY 180 FVQWVGLSPTVWLSVIMMWGFSLYNLSLSPMPLLPFFCLWVYI 227
DB 181 IVQWVAGLSPTVWLSVIMMWGFSLYNLSLSPMPLLPFFCLWVYI 228

RESULT 7
US-08-450-943-3
; Sequence 3, Application US/08450943
; Patent No. 5593825
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLIS, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
```


FILING DATE: 708-938-2623
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-059-031-3

Query Match 93.2%; Score 1194; DB 1; Length 228;
Best Local Similarity 92.1%; Pred. No. 1.7e-106;
Matches 210; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 2 MENIASGLGLPVLVLAQGFLLTKLTIPQSLDSNWTSLNFIPLGGPTVCLGQNSQSSH 61
Db 1 MENTTSGLLGPLLVLAQGFLLTKLTIPQSLDSNWTSLNFIPLGGPTVCLGQNSQSSH 60

QY 62 SPTCCPPICPGYRWMLRRFIIFLCILLCLIFLLVLDYQGMPLVCPPLIPGSSTTSTGP 121
Db 61 SPTCCPPICPGYRWMLRRFIIFLCILLCLIFLLVLDYQGMPLVCPPLIPGSSTTSTGP 120

QY 122 CK--TCTTTPAQTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFSLVLP 179
Db 121 CRNTTCTTTPAQTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFSLVLP 180

QY 180 FVQWFVGLSPTVWLSVINWMMFWGSLYNIILSPFMPLLPIFFCLWYI 227
Db 181 IVQWFAGLSPTVWLSVINWMMFWGSLYNIILSPFMPLLPIFFCLWYI 228

RESULT 9
US-08-450-942-3
Sequence 3, Application US/08450942
Patent No. 5925512
GENERAL INFORMATION:
APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLACE, LESLEY
APPLICANT: MIMMS, LARRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,942
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-942-3

Query Match 93.2%; Score 1194; DB 2; Length 228;
Best Local Similarity 92.1%; Pred. No. 1.7e-106;
Matches 210; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 2 MENIASGLGLPVLVLAQGFLLTKLTIPQSLDSNWTSLNFIPLGGPTVCLGQNSQSSH 61
Db 1 MENTTSGLLGPLLVLAQGFLLTKLTIPQSLDSNWTSLNFIPLGGPTVCLGQNSQSSH 60

QY 62 SPTCCPPICPGYRWMLRRFIIFLCILLCLIFLLVLDYQGMPLVCPPLIPGSSTTSTGP 121
Db 61 SPTCCPPICPGYRWMLRRFIIFLCILLCLIFLLVLDYQGMPLVCPPLIPGSSTTSTGP 120

QY 122 CK--TCTTTPAQTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFSLVLP 179
Db 121 CRNTTCTTTPAQTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFSLVLP 180

QY 180 FVQWFVGLSPTVWLSVINWMMFWGSLYNIILSPFMPLLPIFFCLWYI 227
Db 181 IVQWFAGLSPTVWLSVINWMMFWGSLYNIILSPFMPLLPIFFCLWYI 228

RESULT 10
PCT-US94-05090-3
Sequence 3, Application PC/TUS9405090
GENERAL INFORMATION:
APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLACE, LESLEY
APPLICANT: MIMMS, LARRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05090
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-05090-3

Query Match 93.2%; Score 1194; DB 5; Length 228;
Best Local Similarity 92.1%; Pred. No. 1.7e-106;
Matches 210; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 2 MENIASGLGLLVLAQGFLLTKLTIPQSLDSWMTSLNPLGPGTVCLGQNSQSISS 61
DB 1 MENTTSGLLGLLVLAQGFLLTKLTIPQSLDSWMTSLNPLGPGTVCLGQNSQSISS 60

QY 62 SPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTSTGP 121
DB 61 SPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTSTGP 120

QY 122 CK-TCTTTPAQGTSMFPSCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLVP 179
DB 121 CRNTTCTTTPAQGTSMFPSCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLVP 180

QY 180 FVQWFGLSPTVWLSVIMMMWFMGSPSLYNILSPFMLLPPIFFCLWVYI 227
DB 181 IVQWFGLSPTVWLSVIMMMWFMGSPSLYNILSPFMLLPPIFFCLWVYI 228

RESULT 11
US-08-760-797A-1
; Sequence 1, Application US/08760797A
; Patent No. 5928902
; GENERAL INFORMATION:
; APPLICANT: De Wilde, Michel
; APPLICANT: Cohen, Joseph
; TITLE OF INVENTION: Hybrid Protein Between CS
; TITLE OF INVENTION: from Plasmodium and HBSAG
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,797A
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/442,612
; FILING DATE: 17-MAY-1995
; NAME: Baumeister, Kirk
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: B45015-1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-797A-1

Query Match 92.7%; Score 1187; DB 2; Length 423;
Best Local Similarity 92.1%; Pred. No. 1.6e-105;
Matches 209; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 NMENIASGLGLLVLAQGFLLTKLTIPQSLDSWMTSLNPLGPGTVCLGQNSQSISS 60
DB 188 NMENITSGFLGLLVLAQGFLLTKLTIPQSLDSWMTSLNPLGPGTVCLGQNSQSISS 257

QY 61 HSPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
DB 258 HSPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 317

QY 121 PKTCTTTPAQGTSMFPSCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLVP 180

DB 197 NMENITSGFLGLLVLAQGFLLTKLTIPQSLDSWMTSLNPLGPGTVCLGQNSQSISS 256
QY 61 HSPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
DB 257 HSPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 316
QY 121 PKTCTTTPAQGTSMFPSCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLVP 180
DB 317 PKTCTTTPAQGTSMFPSCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLVP 376

QY 181 VQWFGLSPTVWLSVIMMMWFMGSPSLYNILSPFMLLPPIFFCLWVYI 227
DB 377 VQWFGLSPTVWLSVIMMMWFMGSPSLYNILSPFMLLPPIFFCLWVYI 423

RESULT 12
US-08-760-797A-3
; Sequence 3, Application US/08760797A
; Patent No. 5928902
; GENERAL INFORMATION:
; APPLICANT: De Wilde, Michel
; APPLICANT: Cohen, Joseph
; TITLE OF INVENTION: Hybrid Protein Between CS
; TITLE OF INVENTION: from Plasmodium and HBSAG
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,797A
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/442,612
; FILING DATE: 17-MAY-1995
; NAME: Baumeister, Kirk
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: B45015-1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-797A-3

Query Match 92.7%; Score 1187; DB 2; Length 424;
Best Local Similarity 92.1%; Pred. No. 1.6e-105;
Matches 209; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 NMENIASGLGLLVLAQGFLLTKLTIPQSLDSWMTSLNPLGPGTVCLGQNSQSISS 60
DB 198 NMENITSGFLGLLVLAQGFLLTKLTIPQSLDSWMTSLNPLGPGTVCLGQNSQSISS 257

QY 61 HSPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
DB 258 HSPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 317

QY 121 PKTCTTTPAQGTSMFPSCCTKPTDRNCTCIPSSWAFKYLWENASVRFWSLSLVP 180

Db 318 PKCTCTTAAQNSMFPSCCTKPTDGNCTCIPSSWAFAYLWVWASVRFWSLSLLVVF 377

Qy 181 VQFVGLSPTVWLSAIVMMWVWGSLSYLSIVSPFIPLLPIFFCLWVYI 227

Db 378 VQFVGLSPTVWLSAIVMMWVWGSLSYLSIVSPFIPLLPIFFCLWVYI 424

RESULT 13

US-08-932-929B-1

; Sequence 1, Application US/08932929B

; Patent No. 6169171

; GENERAL INFORMATION:

; APPLICANT: De Wilde, Michel

; TITLE OF INVENTION: Hybrid Protein Between CS

; TITLE OF INVENTION: Hybrid Protein Between CS

; TITLE OF INVENTION: from Plasmodium and HbsAG

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: Fast-Seq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/932,929B

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/760,797

; FILING DATE: 04-DEC-1996

; APPLICATION NUMBER: 08/442,612

; FILING DATE: 17-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Baumeister, Kirk

; REGISTRATION NUMBER: 33,833

; REFERENCE/DOCKET NUMBER: B45015-1FWC2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5096

; TELEFAX: 610-270-5090

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 424 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-932-929B-1

Query Match 92.7%; Score 1187; DB 3; Length 424;

Best Local Similarity 92.1%; Pred. No. 1.6e-105;

Matches 209; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 1 NMENIASGLGLPVLVLAQGFLLTKLTIPQSLDSWWTSLNPLGGPTVCLGQNSQSQISS 60

Db 198 NMENITSGFLGLPVLVLAQGFLLTKLTIPQSLDSWWTSLNPLGGPTVCLGQNSQSPTSN 257

Qy 61 HSPTCCPPICPGVRWMLRRFIIFLCILLCLIFLLVLDYQGMPLPVCPLIPGTTTSTG 120

Db 258 HSPTSCPPICPGVRWMLRRFIIFLCILLCLIFLLVLDYQGMPLPVCPLIPGTTTNTG 317

Qy 121 PKCTCTTAAQNSMFPSCCTKPTDGNCTCIPSSWAFAYLWVWASVRFWSLSLLVVF 180

Db 318 PKCTCTTAAQNSMFPSCCTKPTDGNCTCIPSSWAFAYLWVWASVRFWSLSLLVVF 377

Qy 181 VQFVGLSPTVWLSAIVMMWVWGSLSYLSIVSPFIPLLPIFFCLWVYI 227

Db 378 VQFVGLSPTVWLSAIVMMWVWGSLSYLSIVSPFIPLLPIFFCLWVYI 424

RESULT 15

5196194-21

Db 378 VQFVGLSPTVWLSAIVMMWVWGSLSYLSIVSPFIPLLPIFFCLWVYI 424

RESULT 14

US-08-932-929B-3

; Sequence 3, Application US/08932929B

; Patent No. 6169171

; GENERAL INFORMATION:

; APPLICANT: De Wilde, Michel

; TITLE OF INVENTION: Hybrid Protein Between CS

; TITLE OF INVENTION: Hybrid Protein Between CS

; TITLE OF INVENTION: from Plasmodium and HbsAG

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: Fast-Seq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/932,929B

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/760,797

; FILING DATE: 04-DEC-1996

; APPLICATION NUMBER: 08/442,612

; FILING DATE: 17-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Baumeister, Kirk

; REGISTRATION NUMBER: 33,833

; REFERENCE/DOCKET NUMBER: B45015-1FWC2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5096

; TELEFAX: 610-270-5090

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 424 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-932-929B-3

Query Match 92.7%; Score 1187; DB 3; Length 424;

Best Local Similarity 92.1%; Pred. No. 1.6e-105;

Matches 209; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 1 NMENIASGLGLPVLVLAQGFLLTKLTIPQSLDSWWTSLNPLGGPTVCLGQNSQSQISS 60

Db 198 NMENITSGFLGLPVLVLAQGFLLTKLTIPQSLDSWWTSLNPLGGPTVCLGQNSQSPTSN 257

Qy 61 HSPTCCPPICPGVRWMLRRFIIFLCILLCLIFLLVLDYQGMPLPVCPLIPGTTTSTG 120

Db 258 HSPTSCPPICPGVRWMLRRFIIFLCILLCLIFLLVLDYQGMPLPVCPLIPGTTTNTG 317

Qy 121 PKCTCTTAAQNSMFPSCCTKPTDGNCTCIPSSWAFAYLWVWASVRFWSLSLLVVF 180

Db 318 PKCTCTTAAQNSMFPSCCTKPTDGNCTCIPSSWAFAYLWVWASVRFWSLSLLVVF 377

Qy 181 VQFVGLSPTVWLSAIVMMWVWGSLSYLSIVSPFIPLLPIFFCLWVYI 227

Db 378 VQFVGLSPTVWLSAIVMMWVWGSLSYLSIVSPFIPLLPIFFCLWVYI 424

RESULT 15

5196194-21

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; Patent No. 5196194
; APPLICANT: RUTTER, WILLIAM J.; GOODMAN, HOWARD M.
; TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,621
; FILING DATE: 7-DEC-1984
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 513,055
; FILING DATE: 12-JUL-1983
; APPLICATION NUMBER: 107,267
; FILING DATE: 21-DEC-1979
; APPLICATION NUMBER: 41,909
; FILING DATE: 24-MAY-1979
; SEQ ID NO:21:
; LENGTH: 226
5196194-21

Query Match          92.4%; Score 1184; DB 6; Length 226;
Best Local Similarity 92.5%; Pred. No. 1.5e-105;
Matches 209; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY      2 MENIASGLIGPLLVQAGFFLLTKLTIPQSLDSWTSINFLGGPTVCLGQNSOSQISSH 61
Db      1 MENITSGFLGPLLVQAGFFLLTKLTIPQSLDSWTSINFLGGSPVCLGQNSQSPTSNH 60

QY      62 SPTCCPPICPGYRWMLRRFIIFLCILLCLIFLLVLDYQGLPVCPPIPGSTTTTGP 121
Db      61 SPTSCPPICPGYRWMLRRFIIFLLCLIFLLVLDYQGLPVCPPIPGSTTTTGP 120

QY      122 CKTCTTPAGTSMFFSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFWSLSLLVPFY 181
Db      121 CKTCTTPAGTSMFFSCCCTKPTDGNCCTCIPSSWAFKYLWNASVRFWSLSLLVPFY 180

QY      182 QWFVGLSPTVWLSVIWMWFWGSPSLYNILSPFMPLPIFFCLWYI 227
Db      181 QWFVGLSPTVWLSAIWMWFWGSPSLYSIVSPFIPLLPIFFCLWYI 226
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Search completed: July 26, 2004, 11:30:10
Job time : 27.332 secs

Result No.	Score	Query *		Length	DB	ID	Description
		Match	Quality				
1	1240	96	8	400	14	US-10-224-399A-3461	Sequence 3461, Appl
2	1190	92	9	678	15	US-10-365-820-29	Sequence 29, Appl
3	1190	92.9		678	15	US-10-365-820-32	Sequence 32, Appl
4	1178	92.0		389	14	US-10-169-668-6	Sequence 6, Appl
5	1172	91.5		226	14	US-10-169-668-5	Sequence 5, Appl
6	1164	90.9		281	9	US-09-247-890-12	Sequence 12, Appl
7	1164	90.9		281	15	US-10-383-117-12	Sequence 12, Appl
8	1164	90.9		389	12	US-10-267-682-106	Sequence 106, Appl
9	1164	90.9		389	12	US-10-267-748-106	Sequence 106, Appl
10	1159	90.5		226	16	US-10-335-774-2	Sequence 2, Appl
11	1159	90.5		226	16	US-10-335-774-40	Sequence 40, Appl
12	1159	90.5		389	9	US-09-821-877-2	Sequence 2, Appl
13	1158	90.4		226	9	US-09-929-955-10	Sequence 10, Appl
14	1158	90.4		226	13	US-10-104-966-10	Sequence 10, Appl
15	1158	90.4		226	16	US-10-719-619-10	Sequence 10, Appl

QY 181 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 227
Db 354 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 400

RESULT 2
US-10-365-620-29
; Sequence 29, Application US/10365620
; Publication No. US20040001853A1
; GENERAL INFORMATION:
; APPLICANT: Tyrell, Lorne
; APPLICANT: George, Rajan
; APPLICANT: No. US20040001853A1aim, Antoine
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 656.0016
; CURRENT APPLICATION NUMBER: US/10/365,620
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US60/423,578
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 60/390,564
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-365-620-29

Query Match 92.9%; Score 1190; DB 15; Length 678;
Best Local Similarity 92.5%; Pred. No. 4.1e-95;
Matches 210; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 NMENTASGLGLGLLVQAGFLLTKLTIPOSLSWMTSLNPLGPGTVCLGNSQSQISS 60
Db 202 NMENTSGFLGPLLVQAGFLLTKLTIPOSLSWMTSLNPLGPGTVCLGNSQSQISS 261

QY 61 HSPTCCPPICPGYRMWCLRRRIIFLLCLLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 120
Db 262 HSPTCCPPICPGYRMWCLRRRIIFLLCLLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 321

QY 121 PKCTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLLVPP 180
Db 322 PKCTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLLVPP 381

QY 181 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 227
Db 382 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 428

RESULT 4
US-10-169-668-6
; Sequence 6, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
; APPLICANT: BIOMERIEUX
; APPLICANT: INSERM
; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
; FILE REFERENCE: IFB 99 INS HBVM
; CURRENT APPLICATION NUMBER: US/10/169,668
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-6

Query Match 92.0%; Score 1178; DB 14; Length 389;
Best Local Similarity 90.7%; Pred. No. 2.6e-94;
Matches 206; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 NMENTASGLGLGLLVQAGFLLTKLTIPOSLSWMTSLNPLGPGTVCLGNSQSQISS 60
Db 163 NMENTSGFLGPLLVQAGFLLTKLTIPOSLSWMTSLNPLGPGTVCLGNSQSQISS 222

QY 61 HSPTCCPPICPGYRMWCLRRRIIFLLCLLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 120
Db 223 HSPTCCPPICPGYRMWCLRRRIIFLLCLLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 282

QY 121 PKCTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLLVPP 180
Db 283 PKCTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLLVPP 342

QY 181 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 227
Db 343 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 389

RESULT 5
US-10-169-668-5
; Sequence 5, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
; APPLICANT: BIOMERIEUX
; APPLICANT: INSERM
; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
; FILE REFERENCE: IFB 99 INS HBVM
; CURRENT APPLICATION NUMBER: US/10/169,668
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-5

Query Match 92.0%; Score 1178; DB 14; Length 389;
Best Local Similarity 90.7%; Pred. No. 2.6e-94;
Matches 206; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 NMENTASGLGLGLLVQAGFLLTKLTIPOSLSWMTSLNPLGPGTVCLGNSQSQISS 60
Db 163 NMENTSGFLGPLLVQAGFLLTKLTIPOSLSWMTSLNPLGPGTVCLGNSQSQISS 222

QY 61 HSPTCCPPICPGYRMWCLRRRIIFLLCLLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 120
Db 223 HSPTCCPPICPGYRMWCLRRRIIFLLCLLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 282

QY 121 PKCTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLLVPP 180
Db 283 PKCTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLLVPP 342

QY 181 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 227
Db 343 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 389

RESULT 5
US-10-169-668-5
; Sequence 5, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
; APPLICANT: BIOMERIEUX
; APPLICANT: INSERM
; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
; FILE REFERENCE: IFB 99 INS HBVM
; CURRENT APPLICATION NUMBER: US/10/169,668
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-5

US-10-365-620-32

Query Match 92.9%; Score 1190; DB 15; Length 678;
Best Local Similarity 92.5%; Pred. No. 4.1e-95;
Matches 210; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 NMENTASGLGLGLLVQAGFLLTKLTIPOSLSWMTSLNPLGPGTVCLGNSQSQISS 60
Db 202 NMENTSGFLGPLLVQAGFLLTKLTIPOSLSWMTSLNPLGPGTVCLGNSQSQISS 261

QY 61 HSPTCCPPICPGYRMWCLRRRIIFLLCLLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 120
Db 262 HSPTCCPPICPGYRMWCLRRRIIFLLCLLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 321

QY 121 PKCTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLLVPP 180
Db 322 PKCTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLLVPP 381

QY 181 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 227
Db 382 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 428

RESULT 4
US-10-169-668-6
; Sequence 6, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
; APPLICANT: BIOMERIEUX
; APPLICANT: INSERM
; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
; FILE REFERENCE: IFB 99 INS HBVM
; CURRENT APPLICATION NUMBER: US/10/169,668
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-6

Query Match 92.0%; Score 1178; DB 14; Length 389;
Best Local Similarity 90.7%; Pred. No. 2.6e-94;
Matches 206; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 NMENTASGLGLGLLVQAGFLLTKLTIPOSLSWMTSLNPLGPGTVCLGNSQSQISS 60
Db 163 NMENTSGFLGPLLVQAGFLLTKLTIPOSLSWMTSLNPLGPGTVCLGNSQSQISS 222

QY 61 HSPTCCPPICPGYRMWCLRRRIIFLLCLLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 120
Db 223 HSPTCCPPICPGYRMWCLRRRIIFLLCLLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 282

QY 121 PKCTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLLVPP 180
Db 283 PKCTCTTTPAOGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLLVPP 342

QY 181 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 227
Db 343 VQWFGVLSPTVWLSVIVWMMWFGPSLVNLSPPFMPPLLPFFCLWYI 389

RESULT 5
US-10-169-668-5
; Sequence 5, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
; APPLICANT: BIOMERIEUX
; APPLICANT: INSERM
; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
; FILE REFERENCE: IFB 99 INS HBVM
; CURRENT APPLICATION NUMBER: US/10/169,668
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-5

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/ FILE REFERENCE: IFB 99 INS HBVM
/ CURRENT APPLICATION NUMBER: US/10/169,668
/ CURRENT FILING DATE: 2002-07-08
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 226
/ TYPE: PRT
/ ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-5

Query Match          91.5%; Score 1172; DB 14; Length 226;
Best Local Similarity 90.7%; Pred. No. 5e-94;
Matches 205; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 2 MNENIASGLLGLLVLAGFFLLTKLTIPQSLDSWNTSLNPLGPTVCLGQNSQSQSISS 61
Db 1 MENITSGFLGLLVLAGFFLLTKLTIPQSLDSWNTSLNPLGPTVCLGQNSQSPTS 60

QY 62 SPTCCPPIPCGYRWMCLRRRIIFLCILLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 121
Db 61 SPTSCPPPTCPGYRWMCLRRRIIFLCILLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 120

QY 122 CKTCTTTPAQGTSMPFSCCTKPTDRNCTCIPSSWAFKYLWNASVRFPSWLSLLVPFV 181
Db 121 CRTCTTTPAQGTSMPFSCCTKPSDGNCTCIPSSWAFKFLWNASARFWSLSLLVPFV 180

QY 182 QWFVGLSPTVWLSVIWMWFMGSPSLYNILSPFMPLLPIFFCLWYI 227
Db 181 QWFVGLSPTVWLSVIWMWFMGSPSLYNILRPFLPFLPIFFCLWYI 226

RESULT 6
US-09-247-890-12
; Sequence 12, Application US/09247890
; Publication No. US20020198162A1
; GENERAL INFORMATION:
; APPLICANT: Punnonen, Juha
; APPLICANT: Bass, Steven H.
; APPLICANT: Whalen, Robert Gerald
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Maxygen, Inc.
; TITLE OF INVENTION: Antigen Library Immunization
; FILE REFERENCE: 018097-028710US
; CURRENT APPLICATION NUMBER: US/09/247,890
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,294
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-247-890-12

Query Match          90.9%; Score 1164; DB 9; Length 281;
Best Local Similarity 89.9%; Pred. No. 3.1e-93;
Matches 204; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MNENIASGLLGLLVLAGFFLLTKLTIPQSLDSWNTSLNPLGPTVCLGQNSQSQSISS 60
Db 55 MNENITSGFLGLLVLAGFFLLTKLTIPQSLDSWNTSLNPLGPTVCLGQNSQSP 114

QY 61 HSPTCCPPIPCGYRWMCLRRRIIFLCILLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 120
Db 115 HSPTSCPPPTCPGYRWMCLRRRIIFLCILLCLIFLLVLLDYQGMPLVPCPLIPG 174

QY 121 PKTCTTTPAQGTSMPFSCCTKPTDRNCTCIPSSWAFKYLWNASVRFPSWLSLLVPF 180
Db 175 PCRTCTTTPAQGTSMPFSCCTKPSDGNCTCIPSSWAFKFLWNASARFWSLSLLVPF 234

QY 181 QWFVGLSPTVWLSVIWMWFMGSPSLYNILSPFMPLLPIFFCLWYI 227
Db 235 QWFVGLSPTVWLSVIWMWFMGSPSLYNILRPFLPFLPIFFCLWYI 281

RESULT 7
US-10-383-317-12
; Sequence 12, Application US/10383317
; Publication No. US20040001849A1
; GENERAL INFORMATION:
; APPLICANT: Punnonen, Juha
; APPLICANT: Bass, Steven H.
; APPLICANT: Whalen, Robert Gerald
; APPLICANT: Howard, Russell
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Maxygen, Inc.
; TITLE OF INVENTION: Antigen Library Immunization
; FILE REFERENCE: 018097-028710US
; CURRENT APPLICATION NUMBER: US/10/383,317
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US/09/247,890
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,294
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-383-317-12

Query Match          90.9%; Score 1164; DB 15; Length 281;
Best Local Similarity 89.9%; Pred. No. 3.1e-93;
Matches 204; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MNENIASGLLGLLVLAGFFLLTKLTIPQSLDSWNTSLNPLGPTVCLGQNSQSQSISS 60
Db 55 MNENITSGFLGLLVLAGFFLLTKLTIPQSLDSWNTSLNPLGPTVCLGQNSQSP 114

QY 61 HSPTCCPPIPCGYRWMCLRRRIIFLCILLCLIFLLVLLDYQGMPLVPCPLIPGSTTTSTG 120
Db 115 HSPTSCPPPTCPGYRWMCLRRRIIFLCILLCLIFLLVLLDYQGMPLVPCPLIPG 174

QY 121 PKTCTTTPAQGTSMPFSCCTKPTDRNCTCIPSSWAFKYLWNASVRFPSWLSLLVPF 180
Db 175 PCRTCTTTPAQGTSMPFSCCTKPSDGNCTCIPSSWAFKFLWNASARFWSLSLLVPF 234

QY 181 QWFVGLSPTVWLSVIWMWFMGSPSLYNILSPFMPLLPIFFCLWYI 227
Db 235 QWFVGLSPTVWLSVIWMWFMGSPSLYNILRPFLPFLPIFFCLWYI 281

RESULT 8
US-10-267-682-106
; Sequence 106, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Boicognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 239
```


; PRIOR APPLICATION NUMBER: 09/471,573
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Hepatitis B virus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Wild-type HBsAg amino acid sequence
US-10-335-774-2

Query Match
Best Local Similarity 90.5%; Score 1159; DB 16; Length 226;
Matches 203; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 MENIASGLGLPVLVLAQGFLLTKLTIPQSLDSWMTSLNFGPTVCLGQNSQSQISSH 61
DB 1 MENTTSGFLGLPVLVLAQGFLLTKLTIPQSLDSWMTSLNFGAPTCLGQNSQSPNSH 60

QY 62 SPTCCPPICPGYRWMLRRFIIFCLLLCLIFLLVLDYQGMPLVCPPLPGSTTTSTGP 121
DB 61 SPTSCPPICPGYRWMLRRFIIFCLLLCLIFLLVLDYQGMPLVCPPLPRTSTTSTGP 120

QY 122 CKTCTTPAAGTSMFPSCCCTKPTDRNCTCIPSSWAFAPKYLWENASVRFWSLLVPFV 181
DB 121 CKTCTTPAAGTSMFPSCCCTKPSDGNCTCIPSSWAFARFLWENASVRFWSLLVPFV 180

QY 182 QMFVGLSPTVWLSVIMWMWFGPSLYNLSLSPFLLPIFFCLWVYI 227
DB 181 QMFVGLSPTVWLSVIMWMWFGPSLYNLSLSPFLLPIFFCLWVYI 226

RESULT 11
US-10-335-774-40
; Sequence 40, Application US/10335774
; Publication No. US20040086530A1
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh S.
; TITLE OF INVENTION: Expression of Immunogenic Hepatitis B Surface Antigens In Transgenic Plants
; FILE REFERENCE: 3121/1083
; CURRENT APPLICATION NUMBER: US/10/335,774
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/113,827
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 09/471,573
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 40
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Plant optimized HBsAg amino acid sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: Plant optimized HBsAg amino acid sequence
US-10-335-774-40

Query Match
Best Local Similarity 90.5%; Score 1159; DB 16; Length 226;
Matches 203; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 MENIASGLGLPVLVLAQGFLLTKLTIPQSLDSWMTSLNFGPTVCLGQNSQSQISSH 61
DB 1 MENTTSGFLGLPVLVLAQGFLLTKLTIPQSLDSWMTSLNFGAPTCLGQNSQSPNSH 60

QY 62 SPTCCPPICPGYRWMLRRFIIFCLLLCLIFLLVLDYQGMPLVCPPLPGSTTTSTGP 121

DB 61 SPTSCPPICPGYRWMLRRFIIFCLLLCLIFLLVLDYQGMPLVCPPLPRTSTTSTGP 120
QY 122 CKTCTTPAAGTSMFPSCCCTKPTDRNCTCIPSSWAFAPKYLWENASVRFWSLLVPFV 181
DB 121 CKTCTTPAAGTSMFPSCCCTKPSDGNCTCIPSSWAFARFLWENASVRFWSLLVPFV 180
QY 182 QMFVGLSPTVWLSVIMWMWFGPSLYNLSLSPFLLPIFFCLWVYI 227
DB 181 QMFVGLSPTVWLSVIMWMWFGPSLYNLSLSPFLLPIFFCLWVYI 226

RESULT 12
US-09-821-877-2
; Sequence 2, Application US/09821877
; Patent No. US2002017124A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Coleman, Paul F.
; APPLICANT: Mushahwar, Isa K.
; TITLE OF INVENTION: Hepatitis B Virus Surface Antigen Mutant
; TITLE OF INVENTION: And Methods Of Detection Thereof
; FILE REFERENCE: 6794, US 01
; CURRENT APPLICATION NUMBER: US/09/821,877
; CURRENT FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Hepatitis B Virus
US-09-821-877-2

Query Match
Best Local Similarity 90.5%; Score 1159; DB 9; Length 389;
Matches 204; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 NMENIASGLGLPVLVLAQGFLLTKLTIPQSLDSWMTSLNFGPTVCLGQNSQSQISS 60
DB 163 NMENITSGFLGLPVLVLAQGFLLTKLTIPQSLDSWMTSLNFGPTVCLGQNSQSPNS 222

QY 61 HSTCCPPICPGYRWMLRRFIIFCLLLCLIFLLVLDYQGMPLVCPPLPGSTTTSTG 120
DB 223 HSTSCPPICPGYRWMLRRFIIFCLLLCLIFLLVLDYQGMPLVCPPLPGSTTTSTG 282

QY 121 PKCTTTPAAGTSMFPSCCCTKPTDRNCTCIPSSWAFAPKYLWENASVRFWSLLVPF 180
DB 283 PCRACTTPAAGTSMFPSCCCTKPSDGNCTCIPSSWAFKFLWENASVRFWSLLVPF 342

QY 181 VQMFVGLSPTVWLSVIMWMWFGPSLYNLSLSPFLLPIFFCLWVYI 227
DB 343 VQMFVGLSPTVWLSVIMWMWFGPSLYNLSLSPFLLPIFFCLWVYI 389

RESULT 13
US-09-929-955-10
; Sequence 10, Application US/09929955
; Patent No. US20020136740A1
; GENERAL INFORMATION:
; APPLICANT: Matti Salberg
; APPLICANT: Catharina Hultgren
; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND METHODS OF USE THEREOF
; FILE REFERENCE: TRIPEP-23AUS2
; CURRENT APPLICATION NUMBER: US/09/929,955
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/705,547
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/229,175
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/225,767
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 10
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis B virus S antigen (HBsAg) sequence
US-09-929-955-10

Query Match          90.4%; Score 1158; DB 9; Length 226;
Best Local Similarity 89.8%; Pred. No. 8.2e-93;
Matches 203; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 MENIAGLLGPLLVLAQGFLLTKLTIPQSLDSWNTSLNPLGGPTVCLGQNSQSQISSH 61
Db 1 MENITSGFLGPLLVLAQGFLLTKLTIPQSLDSWNTSLNPLGGPTVCLGQNSQSPTS 60

QY 62 SPTCCPPTCPGYRWNCLRRFIFLCILLCLIFLLVLDYQGMPLVPCPLIPGSTTTSTGP 121
Db 61 SPTSCPPTCPGYRWNCLRRFIFLCILLCLIFLLVLDYQGMPLVPCPLIPGSSTTSTGP 120

QY 122 CKTCTTPAQTSMFPSCCCTKPTDRNCTCIPIPSSWAFKYLWEMASVRFWSLWLLVPFV 181
Db 121 CRTCMWTAQTSMYPSCCCTKPSDGNCTCIPIPSSWAFKGLWEMASARFWSLWLLVPFV 180

QY 182 QWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPFLPLPIFFCLWVYI 227
Db 181 QWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPFLPLPIFFCLWVYI 226

RESULT 14
US-10-104-966-10
; Sequence 10, Application US/10104966
; Publication No. US20020155124A1
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; APPLICANT: Catharina Hultgren
; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
; FILE REFERENCE: TRIPEP.23AUSC1
; CURRENT APPLICATION NUMBER: US/10/104,966
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/705,547
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/229,175
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis B virus S antigen (HBsAg) sequence
US-10-104-966-10

Query Match          90.4%; Score 1158; DB 13; Length 226;
Best Local Similarity 89.8%; Pred. No. 8.2e-93;
Matches 203; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 MENIAGLLGPLLVLAQGFLLTKLTIPQSLDSWNTSLNPLGGPTVCLGQNSQSQISSH 61
Db 1 MENITSGFLGPLLVLAQGFLLTKLTIPQSLDSWNTSLNPLGGPTVCLGQNSQSPTS 60

QY 62 SPTCCPPTCPGYRWNCLRRFIFLCILLCLIFLLVLDYQGMPLVPCPLIPGSTTTSTGP 121
Db 61 SPTSCPPTCPGYRWNCLRRFIFLCILLCLIFLLVLDYQGMPLVPCPLIPGSSTTSTGP 120

QY 122 CKTCTTPAQTSMFPSCCCTKPTDRNCTCIPIPSSWAFKYLWEMASVRFWSLWLLVPFV 181
Db 121 CRTCMWTAQTSMYPSCCCTKPSDGNCTCIPIPSSWAFKGLWEMASARFWSLWLLVPFV 180

QY 182 QWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPFLPLPIFFCLWVYI 227
Db 181 QWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPFLPLPIFFCLWVYI 226
```

```
Db 181 QWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPFLPLPIFFCLWVYI 226

RESULT 15
US-10-719-619-10
; Sequence 10, Application US/10719619
; Publication No. US200400086529A1
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; APPLICANT: Catharina Hultgren
; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
; FILE REFERENCE: TRIPEP.23AUSC1
; CURRENT APPLICATION NUMBER: US/10/719,619
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 10/104,966
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/705,547
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/229,175
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis B virus S antigen (HBsAg) sequence
US-10-719-619-10

Query Match          90.4%; Score 1158; DB 16; Length 226;
Best Local Similarity 89.8%; Pred. No. 8.2e-93;
Matches 203; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 MENIAGLLGPLLVLAQGFLLTKLTIPQSLDSWNTSLNPLGGPTVCLGQNSQSQISSH 61
Db 1 MENITSGFLGPLLVLAQGFLLTKLTIPQSLDSWNTSLNPLGGPTVCLGQNSQSPTS 60

QY 62 SPTCCPPTCPGYRWNCLRRFIFLCILLCLIFLLVLDYQGMPLVPCPLIPGSTTTSTGP 121
Db 61 SPTSCPPTCPGYRWNCLRRFIFLCILLCLIFLLVLDYQGMPLVPCPLIPGSSTTSTGP 120

QY 122 CKTCTTPAQTSMFPSCCCTKPTDRNCTCIPIPSSWAFKYLWEMASVRFWSLWLLVPFV 181
Db 121 CRTCMWTAQTSMYPSCCCTKPSDGNCTCIPIPSSWAFKGLWEMASARFWSLWLLVPFV 180

QY 182 QWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPFLPLPIFFCLWVYI 227
Db 181 QWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPFLPLPIFFCLWVYI 226

Search completed: July 26, 2004, 11:38:30
Job time : 75.456 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2004, 11:23:20 ; Search time 20.884 Seconds
(without alignments)
1045.560 Million cell updates/sec

Title: US-09-719-533A-3_COPY_174_400
Perfect score: 1281
Sequence: 1 NMENIASGLLPVLVQAGF.....NILSPFMPLLPIFFCLWVYI 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.78:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252	97.7	389	1 SAVLJ2	large surface anti
2	1250	97.6	226	2 JQ2057	surface antigen -
3	1247	97.3	389	1 SAVLJ1	large surface anti
4	1246	97.3	226	2 JQ2058	surface antigen -
5	1240	96.8	226	1 JQ1570	major surface anti
6	1240	96.8	226	2 JQ2061	surface antigen -
7	1236	96.5	226	2 JQ2060	surface antigen -
8	1235	96.4	389	1 SAVLJ3	large surface anti
9	1226	95.7	226	2 JQ2059	surface antigen -
10	1219	95.2	226	2 JQ2062	surface antigen -
11	1202	93.8	226	2 JQ2050	surface antigen -
12	1192	93.1	226	2 JQ2052	surface antigen -
13	1190	92.9	400	1 SAVLVD	large surface anti
14	1190	92.9	400	1 JQ1575	major surface anti
15	1189	92.8	226	1 SAVLHV	major surface anti
16	1188	92.7	226	2 JQ2054	surface antigen -
17	1184	92.4	226	1 JQ1577	major surface anti
18	1184	92.4	226	2 JQ2053	surface antigen -
19	1184	92.4	226	2 JQ2051	surface antigen -
20	1180	92.1	226	2 JQ2045	surface antigen -
21	1180	92.1	226	2 JQ2048	surface antigen -
22	1178	92.0	226	2 JQ2055	surface antigen -
23	1178	92.0	389	1 SAVLJH	large surface anti
24	1178	92.0	389	1 SAVLVE	large surface anti
25	1178	92.0	389	2 S20745	surface antigen -
26	1178	92.0	389	2 S20753	surface antigen -
27	1173	91.6	226	2 JQ2046	surface antigen -
28	1170	91.3	226	2 JQ2112	surface antigen -
29	1168	91.2	226	2 JQ2077	surface antigen -

30	1168	91.2	226	2 JQ2076	surface antigen -
31	1168	91.2	226	2 JQ2091	surface antigen -
32	1168	91.2	389	1 SAVLCP	large surface anti
33	1167	91.1	226	2 JQ2110	surface antigen -
34	1167	91.1	226	2 JQ2066	surface antigen -
35	1167	91.1	226	2 JQ2047	surface antigen -
36	1166	91.0	226	1 JQ1571	major surface anti
37	1166	91.0	389	2 S36654	surface antigen -
38	1166	91.0	400	1 SAVLA	large surface anti
39	1165	90.9	226	1 SAVLAD	major surface anti
40	1165	90.9	389	2 S32202	large surface anti
41	1164	90.9	226	2 JQ2079	surface antigen -
42	1164	90.9	226	2 JQ2075	surface antigen -
43	1164	90.9	389	1 SAVLAH	large surface anti
44	1163	90.8	226	2 JQ2078	surface antigen -
45	1163	90.8	226	2 JQ2090	surface antigen -

ALIGNMENTS

RESULT 1

SAVLJ2
large surface antigen - hepatitis B virus (subtype adw, strain Okinawa/podw282)
N:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 14-Nov-1997
C/Accession: H28925
R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosowignojo, R.I.; Imai, M.; Miyakawa, Y.; J. Gen. Virol. 69, 2575-2583, 1988
A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of sur
A:Reference number: JS0253; MUID:89010694; PMID:3171552
A:Accession: H28925
A:Molecule type: DNA
A:Residues: 1-389 <OKA>
A/Cross-references: GB:D00330; NID:g221498
C:Genetics:
A:Gene: pre-S1/pre-S2/S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
F:109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F:164-389/Product: major surface antigen (gene S) #status predicted <MSA>
F:4,112/Binding site: carbohydrate (Asn) #status predicted

Query Match	97.7%;	Score 1252;	DB 1;	Length 389;
Best Local Similarity	97.8%;	Pred. No. 9.9e-33;		
Matches 222;	Conservative 2;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	NMENIASGLLPVLVQAGFLLTKILTIPOSLDSWTSINFLGGTVCGLQNSQSISS	60	
Db	163	NMENIASGLLPVLVQAGFLLTKILTIPOSLDSWTSINFLGGTVCGLQNSQSISS	222	
Qy	61	HSPTCCPPICGYRWMLRRFIIFLCILLLFLVLDYQGMPLVPCPLIPGSTTTSTG	120	
Db	223	HSPTCCPPICGYRWMLRRFIIFLCILLLFLVLDYQGMPLVPCPLIPGSTTTSTG	282	
Qy	121	PKCTCTTTPAGTSMFSCCTKPTDRNCTCIPSSNAFAKYLWNASVRFWSLILVVF	180	
Db	283	PKCTCTTTPAGTSMFSCCTKPTDRNCTCIPSSNAFAKYLWNASVRFWSLILVVF	342	
Qy	181	VQMFVGLSPTVWLSVIMWFWGFSLYNLLSPFCLWVYI	227	
Db	343	VQMFVGLSPTVWLSVIMWFWGFSLYNLLSPFCLWVYI	389	

RESULT 2

JQ2057
surface antigen - hepatitis B virus (subtype adw2, strain Sru)
C:Species: hepatitis B virus, HBV
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C/Accession: JQ2057
R:Norde, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius J. Gen. Virol. 74, 1341-1348, 1993

A:Title: Genetic relatedness of hepatitis B virus strains of diverse geographical origin
 A:Reference number: JQ2044; MUID:93329382; PMID:8336122

A:Contents: genogroup B

A:Accession: JQ2057

A:Molecule type: DNA

A:Residues: 1-226 <NOR>

C:Genetics:

A:Gene: S

C:Superfamily: hepatitis B virus surface antigen

C:Keywords: surface antigen

Query Match 97.6%; Score 1250; DB 2; Length 226;
 Best Local Similarity 98.2%; Pred. No. 9.3e-93;
 Matches 222; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 MENIAGLLGPLLVLQAGFLLTKILTIPOSLSWMTSLNPLGGPTVCLGQNSQSQSISSH 61

Db 1 MENIAGLLGPLLVLQAGFLLTKILTIPOSLSWMTSLNPLGGPTVCLGQNSQSQSISSH 60

QY 62 SPTCCPPICPGYRWMLRRFIFLCILLCLIFLLVLLDYQGMPLVPCPLIPGTTTSTGP 121

Db 61 SPTCCPPICPGYRWMLRRFIFLCILLCLIFLLVLLDYQGMPLVPCPLIPGTTTSTGP 120

QY 122 CKTCTTTPAQGTSWFFSCCTKPTDRNCTCIPIPSSWAFKYLWNASVRFWSLVLVFPV 181

Db 121 CKTCTTTPAQGTSWFFSCCTKPTDRNCTCIPIPSSWAFKYLWNASVRFWSLVLVFPV 180

QY 182 QMFVGLSPTVWLSVIMWMMFGPSLYNLSLSPMPLPIFFCLWVYI 227

Db 181 QMFVGLSPTVWLSVIMWMMFGPSLYNLSLSPMPLPIFFCLWVYI 226

RESULT 3

SAVLJI

large surface antigen - hepatitis B virus (subtype adw, strain Japan/pJDNW233)

C:Species: hepatitis B virus, HBV

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 14-Nov-1997

C:Accession: G28925

R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosowignjo, R.I.; Imai, M.; Miyakawa, Y.; M

J. Gen. Virol. 69, 2575-2583, 1988

A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of sur

A:Reference number: JS0253; MUID:89010694; PMID:3171552

A:Accession: G28925

A:Molecule type: DNA

A:Residues: 1-389 <OKA>

A:Cross-references: GB:D00329; NID:g221497

C:Genetics:

A:Gene: pre-S1/pre-S2/S

C:Superfamily: hepatitis B virus surface antigen

C:Keywords: glycoprotein; surface antigen

F:109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>

F:175-389/Product: major surface antigen (gene S) #status predicted <MSA>

F:4,112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.3%; Score 1247; DB 1; Length 389;

Best Local Similarity 97.4%; Pred. No. 2.5e-92;

Matches 221; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 NMENIAGLLGPLLVLQAGFLLTKILTIPOSLSWMTSLNPLGGPTVCLGQNSQSQSISS 60

Db 163 NMENIAGLLGPLLVLQAGFLLTKILTIPOSLSWMTSLNPLGGPTVCLGQNSQSQSISS 222

QY 61 HSPTCCPPICPGYRWMLRRFIFLCILLCLIFLLVLLDYQGMPLVPCPLIPGTTTSTG 120

Db 223 HSPTCCPPICPGYRWMLRRFIFLCILLCLIFLLVLLDYQGMPLVPCPLIPGTTTSTG 282

QY 121 PKCTCTTTPAQGTSWFFSCCTKPTDRNCTCIPIPSSWAFKYLWNASVRFWSLVLVFP 180

Db 283 PKCTCTTTPAQGTSWFFSCCTKPTDRNCTCIPIPSSWAFKYLWNASVRFWSLVLVFP 342

QY 181 QMFVGLSPTVWLSVIMWMMFGPSLYNLSLSPMPLPIFFCLWVYI 227

"

Db 343 QMFVGLSPTVWLSVIMWMMFGPSLYNLSLSPMPLPIFFCLWVYI 389

RESULT 4

JQ2058

surface antigen - hepatitis B virus (subtype adw2, strain 1764/92)

C:Species: hepatitis B virus, HBV

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: JQ2058

R:Norde, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus,

J. Gen. Virol. 74, 1341-1348, 1993

A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin

A:Reference number: JQ2044; MUID:93329382; PMID:8336122

A:Contents: genogroup B

A:Accession: JQ2058

A:Molecule type: DNA

A:Residues: 1-226 <NOR>

C:Genetics:

A:Gene: S

C:Superfamily: hepatitis B virus surface antigen

C:Keywords: surface antigen

Query Match 97.3%; Score 1246; DB 2; Length 226;

Best Local Similarity 97.8%; Pred. No. 1.9e-92;

Matches 221; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 MENIAGLLGPLLVLQAGFLLTKILTIPOSLSWMTSLNPLGGPTVCLGQNSQSQSISSH 61

Db 1 MENIAGLLGPLLVLQAGFLLTKILTIPOSLSWMTSLNPLGGPTVCLGQNSQSQSISSH 60

QY 62 SPTCCPPICPGYRWMLRRFIFLCILLCLIFLLVLLDYQGMPLVPCPLIPGTTTSTGP 121

Db 61 SPTCCPPICPGYRWMLRRFIFLCILLCLIFLLVLLDYQGMPLVPCPLIPGTTTSTGP 120

QY 122 CKTCTTTPAQGTSWFFSCCTKPTDRNCTCIPIPSSWAFKYLWNASVRFWSLVLVFPV 181

Db 121 CKTCTTTPAQGTSWFFSCCTKPTDRNCTCIPIPSSWAFKYLWNASVRFWSLVLVFPV 180

QY 182 QMFVGLSPTVWLSVIMWMMFGPSLYNLSLSPMPLPIFFCLWVYI 227

Db 181 QMFVGLSPTVWLSVIMWMMFGPSLYNLSLSPMPLPIFFCLWVYI 226

RESULT 5

JQ1570

major surface antigen - hepatitis B virus (subtype ayw1, strain Pl)

C:Species: hepatitis B virus, HBV

A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999

C:Accession: JQ1570

R:Norde, H.; Hammas, B.; Loesdahl, S.; Courouce, A.M.; Magnus, L.O.

J. Gen. Virol. 73, 1201-1208, 1992

A:Title: Comparison of the amino acid sequences of nine different serotypes of hepatitis

A:Reference number: JQ1570; MUID:92268879; PMID:1588323

A:Accession: JQ1570

A:Molecule type: DNA

A:Residues: 1-226 <NOR>

A:Cross-references: GB:X75660; NID:g416078; PIDN:CAA53347.1; PID:g416079

C:Genetics:

A:Gene: S

C:Superfamily: hepatitis B virus surface antigen

C:Keywords: surface antigen

Query Match 96.8%; Score 1240; DB 1; Length 226;

Best Local Similarity 96.9%; Pred. No. 5.9e-92;

Matches 219; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 MENIAGLLGPLLVLQAGFLLTKILTIPOSLSWMTSLNPLGGPTVCLGQNSQSQSISSH 61

Db 1 MENIAGLLGPLLVLQAGFLLTKILTIPOSLSWMTSLNPLGGPTVCLGQNSQSQSISSH 60

QY 62 SPTCCPPICPGYRWMLRRFIFLCILLCLIFLLVLLDYQGMPLVPCPLIPGTTTSTGP 121

"

Db 61 SPTCCPPICPGYRWMLRRFIIFLCIILLCLIFLLVLDYQGMPLVPCPLIPGSSTTSGP 120
Qy 122 CKTCTTTPAQTSMFPSCCCTKPTDRNCTCIPSPSSWAFKYLWNASVRFWSLLVFPV 181
Db 121 CRCTTTPAQTSMFPSCCCTKPTDRNCTCIPSPSSWAFKYLWNASVRFWSLLVFPV 180
Qy 182 QNFVGLSPTVWLSVIMMMFWGSPSLYNILSPFMPPLPIFFCLWVYI 227
Db 181 QNFVGLSPTVWLSVIMMMFWGSPSLYNILSPFMPPLPIFFCLWVYI 226

RESULT 6
JQ2061
surface antigen - hepatitis B virus (subtype ayw1, strain Ngu)
C:Species: hepatitis B virus, HBV
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: JQ2061
R:Norder, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus, J. Gen. Virol. 74, 1341-1348, 1993
A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A:Reference number: JQ2044; PMID:93329382; PMID:8336122
A:Contents: genogroup B
A:Accession: JQ2061
A:Molecule type: DNA
A:Residues: 1-226 <NOR>
C:Genetics:
A:Gene: S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: surface antigen

Query Match 96.8%; Score 1240; DB 2; Length 226;
Best Local Similarity 96.9%; Pred. No. 5.9e-92;
Matches 219; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MENIASGLGLPLVLQAGFLLTKLTIPQSLDSWMTSLNPLGGPTVCLGQNSQSISSH 61
Db 1 MENIASGLGLPLVLQAGFLLTKLTIPQSLDSWMTSLNPLGGPTVCLGQNSQSISSH 60
Qy 62 SPTCCPPICPGYRWMLRRFIIFLCIILLCLIFLLVLDYQGMPLVPCPLIPGSSTTSGP 121
Db 61 SPTCCPPICPGYRWMLRRFIIFLCIILLCLIFLLVLDYQGMPLVPCPLIPGSSTTSGP 120
Qy 122 CKTCTTTPAQTSMFPSCCCTKPTDRNCTCIPSPSSWAFKYLWNASVRFWSLLVFPV 181
Db 121 CRCTTTPAQTSMFPSCCCTKPTDRNCTCIPSPSSWAFKYLWNASVRFWSLLVFPV 180
Qy 182 QNFVGLSPTVWLSVIMMMFWGSPSLYNILSPFMPPLPIFFCLWVYI 227
Db 181 QNFVGLSPTVWLSVIMMMFWGSPSLYNILSPFMPPLPIFFCLWVYI 226

RESULT 7
JQ2060
surface antigen - hepatitis B virus (subtype ayw1, strain Pon)
C:Species: hepatitis B virus, HBV
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: JQ2060
R:Norder, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus, J. Gen. Virol. 74, 1341-1348, 1993
A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A:Reference number: JQ2044; PMID:93329382; PMID:8336122
A:Contents: genogroup B
A:Accession: JQ2060
A:Molecule type: DNA
A:Residues: 1-226 <NOR>
C:Genetics:
A:Gene: S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: surface antigen

Query Match 96.5%; Score 1236; DB 2; Length 226;
Best Local Similarity 96.5%; Pred. No. 1.2e-91;
Matches 219; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MENIASGLGLPLVLQAGFLLTKLTIPQSLDSWMTSLNPLGGPTVCLGQNSQSISSH 61
Db 1 MENIASGLGLPLVLQAGFLLTKLTIPQSLDSWMTSLNPLGGPTVCLGQNSQSISSH 60
Qy 62 SPTCCPPICPGYRWMLRRFIIFLCIILLCLIFLLVLDYQGMPLVPCPLIPGSSTTSGP 121
Db 61 SPTCCPPICPGYRWMLRRFIIFLCIILLCLIFLLVLDYQGMPLVPCPLIPGSSTTSGP 120
Qy 122 CKTCTTTPAQTSMFPSCCCTKPTDRNCTCIPSPSSWAFKYLWNASVRFWSLLVFPV 181
Db 121 CRCTTTPAQTSMFPSCCCTKPTDRNCTCIPSPSSWAFKYLWNASVRFWSLLVFPV 180
Qy 182 QNFVGLSPTVWLSVIMMMFWGSPSLYNILSPFMPPLPIFFCLWVYI 227
Db 181 QNFVGLSPTVWLSVIMMMFWGSPSLYNILSPFMPPLPIFFCLWVYI 226

RESULT 8
SAVLJ3
large surface antigen - hepatitis B virus (subtype adw, strain Indonesia/p1DW420)
N:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 07-May-1999
C:Accession: I28925; PQ0570
R:Okamoto, H.; Tsuda, F.; Sakugawa, H.; Sastrosowignjo, R.I.; Imai, M.; Miyakawa, Y.; J. Gen. Virol. 69, 2575-2583, 1988
A:Title: Typing hepatitis B virus by homology in nucleotide sequence: comparison of sur-
A:Reference number: JS0253; PMID:89010694; PMID:3171552
A:Accession: I28925
A:Molecule type: DNA
A:Residues: 1-389 <OKA>
A:Cross-references: GB:D00331; NID:9221499
A:Experimental source: subtype adw, strain Indonesia/p1DW420
B:Norder, H.; Courouce, A.M.; Magnus, L.O.
J. Gen. Virol. 73, 3141-3145, 1992
A:Title: Molecular basis of hepatitis B virus serotype variations within the four major
A:Reference number: PQ0453; PMID:93107848; PMID:1469353
A:Accession: PQ0570
A:Molecule type: DNA
A:Residues: 264-343 <NOR>
A:Experimental source: subtype adw2, Stru
C:Genetics:
A:Gene: pre-S1/pre-S2/S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
F:109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <BSA>
F:164-389/Product: major surface antigen (gene S) #status predicted <MSA>
F:4.112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.4%; Score 1235; DB 1; Length 389;
Best Local Similarity 96.9%; Pred. No. 2.2e-91;
Matches 220; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 NMENIASGLGLPLVLQAGFLLTKLTIPQSLDSWMTSLNPLGGPTVCLGQNSQSISSH 60
Db 163 NMENIASGLGLPLVLQAGFLLTKLTIPQSLDSWMTSLNPLGGPTVCLGQNSQSISSH 222
Qy 61 HSPTCCPPICPGYRWMLRRFIIFLCIILLCLIFLLVLDYQGMPLVPCPLIPGSSTTSGT 120
Db 223 HSPTCCPPICPGYRWMLRRFIIFLCIILLCLIFLLVLDYQGMPLVPCPLIPGSSTTSGT 282
Qy 121 PKCTCTTTPAQTSMFPSCCCTKPTDRNCTCIPSPSSWAFKYLWNASVRFWSLLVFPV 180
Db 283 PKCTCTTTPAQTSMFPSCCCTKPTDRNCTCIPSPSSWAFKYLWNASVRFWSLLVFPV 342
Qy 181 VQMFVGLSPTVWLSVIMMMFWGSPSLYNILSPFMPPLPIFFCLWVYI 227
Db 343 VQMFVGLSPTVWLSVIMMMFWGSPSLYNILSPFMPPLPIFFCLWVYI 389

RESULT 9
JQ2059

surface antigen - hepatitis B virus (subtype adw2, strain 748/92)
 C:Species: hepatitis B virus, HBV
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: JQ2059
 R:Norder, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus, J. Gen. Virol. 74, 1341-1348, 1993
 A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
 A:Reference number: JQ2044; MUID:93329382; PMID:8336122
 A:Contents: genogroup B
 A:Accession: JQ2059
 A:Molecule type: DNA
 A:Residues: 1-226 <NOR>
 C:Genetics:
 A:Gene: S
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen

Query Match 95.7%; Score 1226; DB 2; Length 226;
 Best Local Similarity 96.0%; Pred. No. 7.7e-91;
 Matches 217; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 2 MENIASGLGLLVLOAGFFLLTKILTIPOSLDSWMTSLNFLGGPTVCLGQNSQSQISSH 61
 DB 1 MENTASGFLGLLVLOAGFFLLTKILTIPOSLDSWMTSLNFLGGPTVCLGQNSQSQISSH 60
 QY 62 SPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVPCFLIPGSTTTSTGP 121
 DB 61 SPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVPCFLIPGSTTTSTGP 120
 QY 122 CKTCTTPAOGTSMFPSCCCTKPTDRNCTCIPSPSWAFKYLWNASVRFWSLSLLVPFV 181
 DB 121 CKTCTTPAOGTSMFPSCCCTKPTDRNCTCIPSPSWAFKYLWNASVRFWSLSLLVPFV 180
 QY 182 QNFVGLSPTVWLSVIMMWFGPSLYNLSLSPFMPILLPIFFCLWVYI 227
 DB 181 QNFVGLSPTVWLSVIMMWFGPSLYNLSLSPFMPILLPIFFCLWVYI 226

RESULT 10
 JQ2062
 surface antigen - hepatitis B virus (subtype ayw1, strains Vut and Meu)
 C:Species: hepatitis B virus, HBV
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: JQ2062; PQ0580
 R:Norder, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus, J. Gen. Virol. 74, 1341-1348, 1993
 A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
 A:Reference number: JQ2044; MUID:93329382; PMID:8336122
 A:Contents: genogroup B
 A:Accession: JQ2062
 A:Molecule type: DNA
 A:Residues: 1-226 <NOR>
 A:Experimental source: strain Vut
 R:Norder, H.; Courouce, A.M.; Magnus, L.O.
 J. Gen. Virol. 73, 3141-3145, 1992
 A:Title: Molecular basis of hepatitis B virus serotype variations within the four major
 A:Reference number: PQ0453; MUID:93107848; PMID:1469353
 A:Accession: PQ0580
 A:Molecule type: DNA
 A:Residues: 101-180 <NO2>
 A:Experimental source: strain Meu
 C:Genetics:
 A:Gene: S
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen

Query Match 95.2%; Score 1219; DB 2; Length 226;
 Best Local Similarity 95.6%; Pred. No. 2.8e-90;
 Matches 216; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 2 MENIASGLGLLVLOAGFFLLTKILTIPOSLDSWMTSLNFLGGPTVCLGQNSQSQISSH 61
 DB 1 MENTASGFLGLLVLOAGFFLLTKILTIPOSLDSWMTSLNFLGGPTVCLGQNSQSQISSH 60

QY 62 SPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVPCFLIPGSTTTSTGP 121
 DB 61 SPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVPCFLIPGSTTTSTGP 120
 QY 122 CKTCTTPAOGTSMFPSCCCTKPTDRNCTCIPSPSWAFKYLWNASVRFWSLSLLVPFV 181
 DB 121 CKTCTTPAOGTSMFPSCCCTKPTDRNCTCIPSPSWAFKYLWNASVRFWSLSLLVPFV 180
 QY 182 QNFVGLSPTVWLSVIMMWFGPSLYNLSLSPFMPILLPIFFCLWVYI 227
 DB 181 QNFVGLSPTVWLSVIMMWFGPSLYNLSLSPFMPILLPIFFCLWVYI 226

RESULT 11
 JQ2050
 surface antigen - hepatitis B virus (subtype adw2, strain 1046/85)
 C:Species: hepatitis B virus, HBV
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: JQ2050
 R:Norder, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus, J. Gen. Virol. 74, 1341-1348, 1993
 A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
 A:Reference number: JQ2044; MUID:93329382; PMID:8336122
 A:Contents: genogroup A
 A:Accession: JQ2050
 A:Molecule type: DNA
 A:Residues: 1-226 <NOR>
 C:Genetics:
 A:Gene: S
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen

Query Match 93.8%; Score 1202; DB 2; Length 226;
 Best Local Similarity 94.2%; Pred. No. 6.3e-89;
 Matches 213; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
 QY 2 MENIASGLGLLVLOAGFFLLTKILTIPOSLDSWMTSLNFLGGPTVCLGQNSQSQISSH 61
 DB 1 MENITSGFLGLLVLOAGFFLLTKILTIPOSLDSWMTSLNFLGGPTVCLGQNSQSQSPTSNH 60
 QY 62 SPTCCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVPCFLIPGSTTTSTGP 121
 DB 61 SPTSCPPICPGYRWMLRRFIIFLCILLLCLIFLLVLDYQGMPLVPCFLIPGSTTTSTGP 120
 QY 122 CKTCTTPAOGTSMFPSCCCTKPTDRNCTCIPSPSWAFKYLWNASVRFWSLSLLVPFV 181
 DB 121 CKTCTTPAOGTSMFPSCCCTKPTDRNCTCIPSPSWAFKYLWNASVRFWSLSLLVPFV 180
 QY 182 QNFVGLSPTVWLSVIMMWFGPSLYNLSLSPFMPILLPIFFCLWVYI 227
 DB 181 QNFVGLSPTVWLSVIMMWFGPSLYNLSLSPFMPILLPIFFCLWVYI 226

RESULT 12
 JQ2052
 surface antigen - hepatitis B virus (subtype adw2, strain 8903/86)
 C:Species: hepatitis B virus, HBV
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: JQ2052
 R:Norder, H.; Hammes, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus, J. Gen. Virol. 74, 1341-1348, 1993
 A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
 A:Reference number: JQ2044; MUID:93329382; PMID:8336122
 A:Contents: genogroup A
 A:Accession: JQ2052
 A:Molecule type: DNA
 A:Residues: 1-226 <NOR>
 C:Genetics:
 A:Gene: S
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen

Query Match 93.1%; Score 1192; DB 2; Length 226;
Best Local Similarity 93.4%; Pred.No.3.9e-88;
Matches 211; Conservative 4; Mismatches 11; Indels 0; Gaps 0

QY	2	MENIASGULLPALLVLQAGFFLLTKLITIPQSLDSWTSINFLGPTVCIGQNSQSOISH	61
Db	1	MENITSGFGLPALLVLQAGFFLLTRILTIPOSLDSWTSINFLGSPVCLGQNSQSPTS	60
QY	62	SPTCCPPICPGYRWCLRRFIIFCIILLCLILFLLVLDYQGMPLVCPILIPGTTTTSTGP	121
Db	61	SPTSCPPICPGYRWCLRRFIIFILLCLILFLLVLDYQGMPLVCPILIPGTTTTSTGP	120
QY	122	CKTCTTPAQGTSMFSCCCTKPTDRNCTCIPIPSSWAFAXYLMEWASVRFWSMLSLLVPPV	181
Db	121	CKTCTTPAQGNSMFSCCCTKPTDGNCTCIPIPSSWAFAXYLMEWASVRFWSMLSLLVPPV	180
QY	182	QMFVGLSPTVWLUSVITWMMWFNGPSLYNILSPFNPILLPIFFCLMVYI	227
Db	181	QMFVGLSPTVWLUSAIWMMWYGPSLYNILSPFIPLLPIFFCLMVYI	226

RESULT 13
SAVLVD
large surface antigen - hepatitis B virus (subtype adw2)
N:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
C:date: 31-Jul-1980 #sequence, revision 14-Nov-1983 #text_change 16-Jul-1999
C:Accession: A03706; C93212; PQ0453; PQ0569
R:Valenzuela, P.; Quiroga, M.; Zaidivar, J.; Gray, P.; Rutter, W.J.
in Animal Virus Genetics, Field, B.N., Jaenisch, R., and Fox, C.F., eds., pp.57-70, Academic Press, New York, 1979
A:Reference number: A94409
A:Accession: A03706
A:Molecule type: DNA
A:Residues: 1-400 <VAL>
R:Valenzuela, P.; Gray, P.; Quiroga, M.; Zaidivar, J.; Goodman, H.M.; Rutter, W.J.
Nature 280, 815-819, 1979
A:title: Nucleotide sequence of the gene coding for the major protein of hepatitis B virus
A:Reference number: A93212; MJUD:79244739; PMID:471053
A:Contents: Dane particles
A:Accession: C93212
A:Molecule type: DNA
A:Residues: 175-400 <VA2>
A:Cross-references: GB:J02205; NID:G929718; PID:AAA45524.1; PID:G929719
A:Note: Dane particles are 42-nm, spherical particulate structures found in the plasma
A:Note: the Dane particle is probably the hepatitis B virion
R:Nordest, H.; Courouce, A.M.; Magnius, L.O.
J. Gen. Virol. 77, 3141-3145, 1992
A:title: Molecular basis of hepatitis B virus serotype variations within the four major
A:Reference number: PQ0453; MJUD:93107848; PMID:1469353

Query Match 92.9%; Score 1190; DB 1; Length 400;
Best Local Similarity 92.5%; Pred. No. 8.9e-88;
Matches 210; Conservative 6; Mismatches 11; Indels 0; Gaps 0

```

QY      1 NMENIASGLGPLVLVLAQGFLLTKILTIPOSLSWWTSLNFLGPTVCLGQNSQSQISS 60
      |||||
      174 NMENITSGPLVLVLAQGFLLTKILTIPOSLSWWTSLNFLGSPVCLGQNSQPSITSN 233
      |||||

```

QY	61	HSPTCCPPICGRYWNCMLRRRIIFCLILLICLLFLVLLDYQGMFLPVCPLIPGSTTTSTG	120
Db	234	HSPTCCPPICGRYWNCMLRRRIIFCLILLICLLFLVLLDYQGMFLPVCPLIPGSTTTSTG	293
QY	121	PCKTCTTTPAQISMPPPSCCTCKPTDRNCTCIPISSSWAFKAKYLWEMASVRFSLSLVLP	180
Db	294	PCKTCTTTPAQNSMPPPSCCTCKPTDGNCTCIPISSSWAFKAKYLWEMASVRFSLSLVLP	353
QY	181	VQVFGVGLSPTVMLSIVYMMWFGVSGSLYNIISPEMPLPIFFCLMWYI	227
Db	354	VQVFGVGLSPTVMLSAIMWMMWFGVSGSLYSIVSPFIPLPIFFCLMWYI	400

RESULT 14

major surface antigen - hepatitis B virus

major surface antigen - hepatitis B virus

N;Alternate names: envelope protein; HBs antigen

N;Contains: surface antigen pre-s1 (large envelope protein); surface antigen pre-s2 (mi

C;Species: hepatitis B virus, HBV

A;Variety: subtype adw2

C;Date: 31-Dec-1993 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

A;Accession: S47411; JQ1575

R;Plucienniczak, A.

submitted to the EMBL Data Library, August 1994

A;Description: Molecular cloning and sequencing of two complete genomes of poliovirus isolates

A;Reference number: S47404

A;Accession: S47411

A;Molecule type: DNA

A;Residues: 1-400 <PLU>

A;Cross-references: EMBL:Z35717; NID:G527440; PIDN:CAA84792.1; PID:G527444

A;Experimental source: subtype adw2

R;Norder, H.; Hammas, B.; Loeferthal, S.; Courouce, A.M.; Magnius, L.O.

J. Gen. Virol. 73, 1201-1208, 1992

A;Title: Comparison of the amino acid sequences of nine different serotypes of hepatitis B virus

A;Reference number: JQ1570; MUID:92268879; PMID:1568323

A;Accession: JQ1575

A;Molecule type: DNA

A;Residues: 175-400 <NOR>

A;Cross-references: GB:X758666; NID:G416074; PIDN:CAAS3362.1; PID:G416075

A;Experimental source: subtype adw2, strain P6

Query Match	92.9%;	Score 1190;	DB 1;	Length 400;
Best Local Similarity	92.5%;	Pred. No. 8.9e-88;		
Matches 210; Conservative	6;	Mismatches 11;	Indels 0;	Gaps 0

```
QY      1 NMENIAGLLGPLVLQAGFFLLTKILTIPOSLDSSWWTISNLFGLGPTVCLGNSQSQISS 60
        ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     174 NMENITGGFLGPLVLQAGFFLLTRILTIPOSLDSSWWTISNLFGLGSPVCIGNSOSQPSN 233
```

QY	61	HSPTCCPPI	CGYRWKCLRRRIIFELCLILLCLFLFLLVLDYQGLWPCVPLIPGSTTTSTG	120
Db	234	HSPTSCPPI	CGYRWKCLRRRIIFELCLILLCLFLFLLVLDYQGLWPCVPLIPGSTTTSTG	293
QY	121	PCKTCTT	PAQGTSMFPSCCCTKPTDRNCTCIPSSWAFAKYLWEMASVRFSLSLVLPF	180
Db	294	PCKTCTT	PAQGNMFPSCCCTKPTDGNCTCIPSSWAFAKYLWEMASVRFSLSLVLPF	353
QY	181	VQWVGLSPT	VMLSVIWMWFMGSLYNILSPFWLLPIEFCLWVII	227
Db	354	VQWVGLSPT	VMLSAIWMWYWGSLYSIVSRPIPLPIEFCLWVI	400

```
RESULT 15
SAVLHV
Major surface antigen - hepatitis B virus
C:Species: hepatitis B virus, HBV
A:Note: host Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C:Accession: J02993
R:Rivkina, M.B.; Lunin, V.G.; Mahov, A.M.; Tikhonenko, T.I.; Kukain, R.A.
Gene 64, 285-296, 1988
A:Title: Nucleotide sequence of integrated hepatitis B virus DNA and human flanking regi
A:Reference number: J02993; MUID:88297159; PMID:2841200
A:Accession: J02993
A:Molecule type: DNA
A:Residues: 1-226 <RIV>
A:Cross-references: GB:M21030; NID:g329702; PIDN:AAA45516.1; PID:g329703
C:Genetics:
A:Gene: S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
F3/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      92.8%; Score 1189; DB 1; Length 226;
Best Local Similarity 92.9%; Pred. No. 6.8e-88;
Matches 210; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 MENIASGLLPVLVQAGFELLTKLTIPQSLDSWWTSLNFI LGGPTVCLGQNSQSISSH 61
Db 1 MENITSGFLGPLVLVQAGFELLTRLTIPQSLDSWWTSLNFI LGGSPVCLGQNSQSPTSNH 60

QY 62 SPTCCPPICPGYRMMCLRRFIFLCILLCLIFLLVLLDYQGM LFPVCP LIPGSTTTSTGP 121
Db 61 SPTSCPPICPGYRMMCLRRFIFLFILLCLIFLLVLLDYQGM LFPVCP LIPGSTTTSTGP 120

QY 122 CXTCTTPAQTSMFPSCCCTKPTDNCCTCIPISWAFKYLWENASVRFPSWLSLLVPFV 181
Db 121 CXTCTTPAQTSMFPSCCCTKPTDNCCTCIPISWAFKYLWENASVRFPSWLSLLVPFV 180

QY 182 QWFVGLSPTVWLSVIWMWFWGPSLYNLSPPMPLPIFFCLWVYI 227
Db 181 QWFVGLSPTVWLSVIWMWFWGNLYNLSPPFIPPLPIFFCLWVYI 226
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Search completed: July 26, 2004, 11:29:29
Job time : 20.884 secs

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OM protein - protein search, using sw model

Run on: July 26, 2004, 11:13:24 ; Search time 14.528 Seconds
(without alignments)
813.596 Million cell updates/sec

Title: US-09-719-533A-3_COPY_174_400
Perfect score: 1281
Sequence: 1 NMENIASGLGLVQLQAGF.....NILSPFMPLLPIPFCLWYVI 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252	97.7	389	1 VMSA_HPBVO	P17399 hepatitis b
2	1247	97.3	389	1 VMSA_HPBVO	P17398 hepatitis b
3	1235	96.4	389	1 VMSA_HPBVI	P17397 hepatitis b
4	1198	93.5	400	1 VMSA_HPBVP	Q02317 hepatitis b
5	1190	92.9	400	1 VMSA_HPBVP	P03141 hepatitis b
6	1189	92.8	226	1 VMSA_HPBVO	P31873 hepatitis b
7	1178	92.0	389	1 VMSA_HPBVO	P31873 hepatitis b
8	1168	91.2	389	1 VMSA_HPBVL	P31873 hepatitis b
9	1166	91.0	400	1 VMSA_HPBVR	P31873 hepatitis b
10	1165	90.9	389	1 VMSA_HPBVD	P31868 hepatitis b
11	1164	90.9	389	1 VMSA_HPBVD	P31868 hepatitis b
12	1162	90.7	389	1 VMSA_HPBVA	P24025 hepatitis b
13	1161	90.6	400	1 VMSA_HPBVA	P17101 hepatitis b
14	1159	90.5	226	1 VMSA_HPBVN	P30019 hepatitis b
15	1159	90.5	389	1 VMSA_HPBVZ	P30019 hepatitis b
16	1153	90.0	400	1 VMSA_HPBVZ	P30019 hepatitis b
17	1148	89.6	226	1 VMSA_HPBVS	P12934 hepatitis b
18	1062	82.9	400	1 VMSA_HPBVT	P31869 hepatitis b
19	769	60.0	428	1 VMSA_HPBGS	Q05496 hepatitis b
20	763	59.6	431	1 VMSA_HBV59	P03144 ground squi
21	761	59.4	431	1 VMSA_HBV7	P12910 woodchuck h
22	759	59.3	431	1 VMSA_HBV8I	P12909 woodchuck h
23	758	59.2	426	1 VMSA_HBVW6	P17400 woodchuck h
24	755	58.9	282	1 VMSA_HBVW1	P11293 woodchuck h
25	742	57.9	431	1 VMSA_HBV8	P03143 woodchuck h
26	202.5	15.8	328	1 VMSA_HPB8U	P06432 woodchuck h
27	201.5	15.7	366	1 VMSA_HPBDM	P03145 duck hepati
28	197.5	15.4	365	1 VMSA_HPBDC	P17195 duck hepati
29	196	15.3	335	1 VMSA_HPBDC	P30029 duck hepati
30	195.5	15.3	366	1 VMSA_HPBHE	P13847 heron hepat
31	102	8.0	363	1 VMSA_HPBDB	P17194 duck hepati
32	100	7.8	251	1 K10A_HUMAN	P00164 trypanosoma
33	92.5	7.2	784	1 YAV2_XANCV	P60014 homo sapien
					P14728 xanthomonas

ALIGNMENTS

RESULT 1

VMSA_HPBVO
ID VMSA_HPBVO STANDARD; PRT; 389 AA.
AC P17399;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adv / strain Okinawa/pODW282).
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID:10415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89010694; PubMed=3171552;
RA Okamoto H., Tsuda F., Sakagawa H., Sastrosowigno R.I., Imai M.,
Miyakawa Y., Mayumi M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes.";
RL J. Gen. Virol. 69:2575-2583(1988).
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DR EMBL; D00330; -; NOT_ANNOTATED_CDS.
DR FIR; H28925; SAVL02.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 163
FT CHAIN 164 389 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 389 AA; 42408 MW; CECACODDA3D84A10 CRC64;

Query Match

Best Local Similarity 97.7%; Score 1252; DB 1; Length 389;

Matches 222; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMENIASGLGLVQLQAGFFLLTKILITPQSLDSWMTSLNFGPTVCLGNSQSQISS 60
Db 163 NMENIASGLGLVQLQAGFFLLTKILITPQSLDSWMTSLNFGPTVCLGNSQSQISS 222
QY 61 HSPTCCPPTCPGYRWMLRRFIIFCLILLCLIFLLVLLDYQGMPLPVCPPIPGSTTTSTG 120
Db 223 HSPTCCPPTCPGYRWMLRRFIIFCLILLCLIFLLVLLDYQGMPLPVCPPIPGSTTTSTG 282
QY 121 PKCTCTTPAQGSMFPPSCCTKPTDRNCTCIPSSWAFAYLWEMWASRRFSMLSLVVPF 180

RP SEQUENCE FROM N.A.
RA Estacio R.C., Chavez C.C., Okamoto H., Lingao A.L., Reyes M.T.,
RA Domingo E., Mayumi M.,
RT "Nucleotide sequence of a hepatitis B virus genome of subtype adw
RT isolated from a Filipino: comparison with the reported three genomes
of the same subtype.";
RL J. Gastroenterol. Hepatol. 3:215-222 (1988).
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CC -----
DR EMBL; M57663; AAA69680.1; -;
DR InterPro; IPR000349; Hepvir_surflag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 174
FT CHAIN 175 400 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 15 15 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 400 AA; 43740 MW; 78BD53A004136BD2 CRC64;
Query Match 93.5%; Score 1198; DB 1; Length 400;
Best Local Similarity 93.4%; Pred. No. 6e-96;
Matches 212; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1 NMENIASGLLGLPVLVLAQAGFFLLTKLTIPQSLDSWNTSLNPLGPGTVCGLGNSQSQIS 60
DB 174 NMENITSGFLGLPVLVLAQAGFFLLTKLTIPQSLDSWNTSLNPLGPGTVCGLGNSQSPTSN 233
QY 61 HSPCTCCPPICGYRWMLCRRRIIFLCILLCLIFLLVLDYQGMPLVPCPLIPGTTTSTG 120
DB 234 HSPCTCCPPICGYRWMLCRRRIIFLCILLCLIFLLVLDYQGMPLVPCPLIPGTTTSTG 293
QY 121 PKCTCTTAQGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWEMASVRFWSLSLLVPF 180
DB 294 PKCTCTTAQGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWEMASVRFWSLSLLVPF 353
QY 181 VQMFVGLSPTVLSVITWMMWFGSLYNILSPFELLPIFFCLWYI 227
DB 354 VQMFVGLSPTVLSVITWMMWFGSLYNILSPFELLPIFFCLWYI 400
RESULT 5
VMSA_HPBV2
ID VMSA_HPBV2 STANDARD; PRT; 400 AA.
AC F03141;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw2).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10408;
RN [1]
RP SEQUENCE FROM N.A.
RA Valenzuela P., Quiroga M., Zaldivar J., Gray P., Rutter W.J.;
RL (In) Field B.N., Jaenisch R., Fox C.F. (eds.);
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).
RN [2]
RN SEQUENCE OF 175-400 FROM N.A.
RX MEDLINE=7924739; PubMed=471053;
RA Valenzuela P., Gray P., Quiroga M., Zaldivar J., Goodman H.M.,
RA Rutter W.J.;
RT "Nucleotide sequence of the gene coding for the major protein of
hepatitis B virus surface antigen.";

RL Nature 280:815-819 (1979).
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CC -----
DR EMBL; X02763; CAA26539.1; -;
DR EMBL; J02205; AAA45524.1; -;
DR FIR; A03706; SAVLVD.
DR InterPro; IPR000349; Hepvir_surflag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 174
FT CHAIN 175 400 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 15 15 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 400 AA; 43704 MW; 57356B6293872BC5 CRC64;
Query Match 92.9%; Score 1190; DB 1; Length 400;
Best Local Similarity 92.5%; Pred. No. 2.9e-95;
Matches 210; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
QY 1 NMENIASGLLGLPVLVLAQAGFFLLTKLTIPQSLDSWNTSLNPLGPGTVCGLGNSQSQIS 60
DB 174 NMENITSGFLGLPVLVLAQAGFFLLTKLTIPQSLDSWNTSLNPLGPGTVCGLGNSQSPTSN 233
QY 61 HSPCTCCPPICGYRWMLCRRRIIFLCILLCLIFLLVLDYQGMPLVPCPLIPGTTTSTG 120
DB 234 HSPCTCCPPICGYRWMLCRRRIIFLCILLCLIFLLVLDYQGMPLVPCPLIPGTTTSTG 293
QY 121 PKCTCTTAQGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWEMASVRFWSLSLLVPF 180
DB 294 PKCTCTTAQGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWEMASVRFWSLSLLVPF 353
QY 181 VQMFVGLSPTVLSVITWMMWFGSLYNILSPFELLPIFFCLWYI 227
DB 354 VQMFVGLSPTVLSVITWMMWFGSLYNILSPFELLPIFFCLWYI 400
RESULT 6
VMSA_HPBV0
ID VMSA_HPBV0 STANDARD; PRT; 226 AA.
AC P31873;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88297159; PubMed=2841200;
RA Rivkina M.B., Lunin V.G., Manov A.M., Tikhonenko T.I., Kukain R.A.;
RT "Nucleotide sequence of integrated hepatitis B virus DNA and human
RT flanking regions in the genome of the PLC/PRF/5 cell line.";
RL Gene 64:285-296 (1988).
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DR EMBL; M21030; AAA45516.1; -;
 DR EMBL; X04820; CAA28506.1; -;
 DR PIR; JTO293; SAVLHV.
 DR InterPro; IPR000349; Hepvir_surfa.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 FT CARBOHYD 3 3 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 226 AA; 25476 MW; BFC4329CF1720600 CRC64;

Query Match 92.8%; Score 1189; DB 1; Length 226;
 Best Local Similarity 92.9%; Pred. No. 2.1e-95;
 Matches 210; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 MENIASGLLGLPLVLQAGFFLLTKILTIPOSLSDSWTSNLFGLGPTVCLGQNSQSISSH 61
 DB 1 MENITSGFLGLPLVLQAGFFLLTKILTIPOSLSDSWTSNLFGLGPTVCLGQNSQSISSH 60
 QY 62 SPTCCPPICPGYRWMCLRRFIIFLCILLLCLIFLLVLDYQGLMPVCPPLIPGTTTSTGP 121
 DB 61 SPTCCPPICPGYRWMCLRRFIIFLCILLLCLIFLLVLDYQGLMPVCPPLIPGTTTSTGP 120
 QY 122 CKTCTTPAAGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFWSLSLLVPFV 181
 DB 121 CKTCTTPAAGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFWSLSLLVPFV 180
 QY 182 QMFVGLSPTVWLSVIMWMMWFGPSLYNLSPPMPLPIPFCLWYI 227
 DB 181 QMFVGLSPTVWLSVIMWMMWFGPSLYNLSPPMPLPIPFCLWYI 226

RESULT 7

VMSA_HPBWV
 ID_VMSA_HPBWV STANDARD; PRT; 389 AA.
 AC P03142;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Major surface antigen precursor.
 GN S.
 OS Hepatitis B virus (subtype adv).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=106821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=83168919; PubMed=6300776;
 RX Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
 RT "The complete nucleotide sequences of the cloned hepatitis B virus
 DNA; subtype adr and adv.";
 RL Nucleic Acids Res. 11:1747-1757 (1983).

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 DR EMBL; V00866; CAA24233.1; ALT_INIT.
 DR PIR; A93460; SAVLVE.
 DR InterPro; IPR000349; Hepvir_surfa.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 FT PROPEP 1 163
 FT CHAIN 164 389
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 389 AA; 42354 MW; FE9EF2E7EEFC58B5 CRC64;

Query Match 92.0%; Score 1178; DB 1; Length 389;
 Best Local Similarity 92.0%; Pred. No. 3e-94;
 Matches 208; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 2 MENIASGLLGLPLVLQAGFFLLTKILTIPOSLSDSWTSNLFGLGPTVCLGQNSQSISSH 61
 DB 164 MENITSGFLGLPLVLQAGFFLLTKILTIPOSLSDSWTSNLFGLGPTVCLGQNSQSISSH 223
 QY 62 SPTCCPPICPGYRWMCLRRFIIFLCILLLCLIFLLVLDYQGLMPVCPPLIPGTTTSTGP 121
 DB 224 SPTCCPPICPGYRWMCLRRFIIFLCILLLCLIFLLVLDYQGLMPVCPPLIPGTTTSTGP 283
 QY 122 CKTCTTPAAGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFWSLSLLVPFV 181
 DB 284 CKTCTTPAAGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWNASVRFWSLSLLVPFV 343
 QY 182 QMFVGLSPTVWLSVIMWMMWFGPSLYNLSPPMPLPIPFCLWYI 227
 DB 344 QMFVGLSPTVWLSVIMWMMWFGPSLYNLSPPMPLPIPFCLWYI 389

RESULT 8

VMSA_HPBVL
 ID_VMSA_HPBVL STANDARD; PRT; 389 AA.
 AC P12911;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE Major surface antigen precursor.
 GN S.
 OS Hepatitis B virus (strain lsh / chimpanzee isolate).
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10414;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=88258473; PubMed=2838576;
 RX Vaudin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
 RA Harrison T.J.;
 RT "The complete nucleotide sequence of the genome of a hepatitis B
 virus isolated from a naturally infected chimpanzee.";
 RL J. Gen. Virol. 69:1383-1389 (1988).

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 DR EMBL; D00220; BAA00159.1; -;
 DR PIR; C28885; SAVLCP.
 DR InterPro; IPR000349; Hepvir_surfa.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 FT PROPEP 1 163
 FT CHAIN 164 389
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 389 AA; 42539 MW; 87D1F93382A10BDC CRC64;

Query Match 91.2%; Score 1168; DB 1; Length 389;
 Best Local Similarity 90.3%; Pred. No. 2.2e-93;
 Matches 205; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 NMENTASGLLGLPLVLQAGFFLLTKILTIPOSLSDSWTSNLFGLGPTVCLGQNSQSISSH 60
 DB 163 NMENTITSGFLGLPLVLQAGFFLLTKILTIPOSLSDSWTSNLFGLGPTVCLGQNSQSISSH 222
 QY 61 HSPTCCPPICPGYRWMCLRRFIIFLCILLLCLIFLLVLDYQGLMPVCPPLIPGTTTSTGP 120

```
Db 223 HSPTSCPPICPGYRMCLRRFIIFLLFIILLVLLDYOQMLPVCPLIPGSGTTSTG 282
Qy 121 PKCTCTTPAQGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWEMASVRFSLVLPF 190
Db 283 PKCTCTTPAQGTSMFPSCCCTKPSDGNCTCIPSSWAFKYLWEMASVRFSLVLPF 342
Qy 181 VQWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPFMPFLPIFFCLWYI 227
Db 343 VQWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPFMPFLPIFFCLWYI 389

RESULT 9
VMSA HPBVR
ID VMSA HPBVR STANDARD; PRT; 400 AA.
AC P03140;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adr).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=106820;
RN [1]
RP MEDLINE=83168319; PubMed=6300776;
RX Ono Y., Onda H., Sasaki R., Igarashi K., Sugino Y., Nishioka K.;
RA "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adr.";
RL Nucleic Acids Res. 11:1747-1757(1983).
RN [2]
RP SEQUENCE OF 176-350 FROM N.A.
RX MEDLINE=85107103; PubMed=3968537;
RA Tsuchihata H., Inokoshi J., Namiki M., Shimada J., Omura S.;
RT "Structural analysis of the gene coding for hepatitis B virus surface
RT antigen and its product.";
RL J. Gen. Virol. 66:195-200(1985).
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CC -----
DR EMBL; V00867; CAA24234.1; ALT_INIT.
DR PIR; A03705; SAVLA.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 174
FT CHAIN 175 400 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 15 15 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 400 AA; 43685 MW; 16D80B15C6B697A CRC64;

Query Match 91.0%; Score 1166; DB 1; Length 400;
Best Local Similarity 89.9%; Pred. No. 3.4e-93;
Matches 204; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 NMENIASGLLGLPLVLOAGFFLLTKILTIPOSLSWMTSLNFLGGPTVCLGQNSQSIS 60
Db 174 NMENITSGFLGPLLVLOAGFFLLTRILTIPOSLSWMTSLNFLGGAPTCPGQNSQSP 233
Qy 61 HSPTCCPPICPGYRMCLRRFIIFLLFIILLVLLDYOQMLPVCPLIPGSGTTSTG 120
Db 234 HSPTSCPPICPGYRMCLRRFIIFLLFIILLVLLDYOQMLPVCPLIPGSGTTSTG 293
Qy 121 PKCTCTTPAQGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWEMASVRFSLVLPF 180
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Db 294 PKCTCTTPAQGTSMFPSCCCTKPSDGNCTCIPSSWAFKYLWEMASVRFSLVLPF 353
Qy 181 VQWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPFMPFLPIFFCLWYI 227
Db 354 VQWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPFMPFLPIFFCLWYI 400

RESULT 10
VMSA HPBVD
ID VMSA HPBVD STANDARD; PRT; 226 AA.
AC P31858;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus (subtype ad).
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31511;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89143494; PubMed=2465492;
RA Okamoto H., Omi S., Wang Y., Itch Y., Tsuda F., Tanaka T., Akahane Y.,
RA Miyakawa Y., Mayumi M.;
RT "The loss of subtypic determinants in alleles, d/y or w/r, on
RL Mol. Immunol. 26:197-205(1989).
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CC -----
DR EMBL; M27765; AAA45518.1; -.
DR PIR; PL0053; SAVLAD.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 226 AA; 25348 MW; AFC12BCF3B08DC83 CRC64;

Query Match 90.9%; Score 1165; DB 1; Length 226;
Best Local Similarity 90.3%; Pred. No. 2.4e-93;
Matches 204; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 2 MENIASGLLGLPLVLOAGFFLLTKILTIPOSLSWMTSLNFLGGPTVCLGQNSQSIS 61
Db 1 MENITSGFLGPLLVLOAGFFLLTRILTIPOSLSWMTSLNFLGGAPTCPGQNSQSP 60
Qy 62 SPTCCPPICPGYRMCLRRFIIFLLFIILLVLLDYOQMLPVCPLIPGSGTTSTG 121
Db 61 SPTSCPPICPGYRMCLRRFIIFLLFIILLVLLDYOQMLPVCPLIPGSGTTSTG 120
Qy 122 CKTCTTTPAQGTSMFPSCCCTKPTDRNCTCIPSSWAFKYLWEMASVRFSLVLPF 181
Db 121 CKTCTTTPAQGTSMFPSCCCTKPSDGNCTCIPSSWAFKYLWEMASVRFSLVLPF 180
Qy 182 QWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPFMPFLPIFFCLWYI 227
Db 181 QWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPFMPFLPIFFCLWYI 226

RESULT 11
VMSA HPBVI
ID VMSA HPBVI STANDARD; PRT; 389 AA.
AC P03138;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
```

DE Major surface antigen precursor.
GN S.
OC Hepatitis B virus (subtype ayw).
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012091; PubMed=393327;
RA Galibert F., Mandart E., Fricoussi F., Tiollais P., Charnay P.;
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
cloned in E. coli.";
RL Nature 281:646-650(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85204397; PubMed=3996597;
RA Bichko V., Pushko P., Dreilina D., Pumpen P., Gren E.Y.;
RT "Subtype ayw variant of hepatitis B virus. DNA primary structure
analysis.";
RL FEBS Lett. 185:208-212(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Latvia;
RA Pumpen P., Kozlovskaya T.M., Borisova G.L., Byachko V.V.,
RA Dishler A.V., Kalic Y.V., Pudova N.V., Gren E.Y., Krievina V.Y.,
RA Kukain R.A.;
RT "Synthesis of the surface antigen of hepatitis B virus in Escherichia
coli.";
RL Dokl. Biochem. 271:246-249(1984).
RN [4]
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
DR EMBL; V01460; -; NOT ANNOTATED CDS.
DR EMBL; X02496; AAA26324.1; ALT INIT.
DR EMBL; M12393; AAA45496.1; ALT_INIT.
DR PIR; A03703; SAVLAH.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; vmsa; 1.
KW Antigen.
FT PROPEP 1 163
FT CHAIN 164 389 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 75 75 Q -> E (IN STRAIN LATVIA).
FT VARIANT 147 147 A -> S (IN STRAIN LATVIA).
FT VARIANT 150 150 L -> I (IN STRAIN LATVIA).
FT VARIANT 288 288 MTT -> TTP (IN STRAIN LATVIA).
SQ SEQUENCE 389 AA; 42766 MW; 6DC9B682DA634F63 CRC64;
Query Match 90.9%; Score 1164; DB 1; Length 389;
Best Local Similarity 89.9%; Pred. No. 4.9e-93;
Matches 204; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
QY 1 NMENIASGLGLPLVLQAGFLLTKILTIPOSLSWTSNLFGLGPTVCLGNSQSISS 60
DB 163 NMENITSGFLGLPLVLQAGFLLTKILTIPOSLSWTSNLFGLGTTVCLGNSQSPSTN 222
QY 61 HSPTCCPPICGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
DB 223 HSPTSCPTCPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 282
QY 121 PKCTCTTAAQGTSMFPCSCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLPV 180
DB 283 PCRTMTAQTSMYPCSCCTKPSDGNCTCIPSSWAFKFLWENASVRFSLVLPV 342

QY 181 VQMFVGLSPTVWLSVIMWMWFWGSPSLYNILSPFMPPLPIPFCLWVYI 227
DB 343 VQMFVGLSPTVWLSVIMWMWFWGSPSLYNILSPFMPPLPIPFCLWVYI 389
RESULT 12
VMSA HPBVA
ID VMSA HPBVA STANDARD; PRT; 389 AA.
AC P24025;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (strain alphas).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10411;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90286476; PubMed=2345966;
RA Tong S., Li J., Vitvitski L., Trepo C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is
associated with viral variants containing an inactive pre-C region.";
RL Virology 176:596-603(1990).
RN [2]
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DR EMBL; M32138; AAA45502.1; -
DR PIR; B34773; SAVLAH.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; vmsa; 1.
KW Antigen.
FT PROPEP 1 163
FT CHAIN 164 389 MAJOR SURFACE ANTIGEN.
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 389 AA; 42733 MW; B806D0D42B23BF5 CRC64;
Query Match 90.7%; Score 1162; DB 1; Length 389;
Best Local Similarity 89.4%; Pred. No. 7.2e-93;
Matches 203; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
QY 1 NMENIASGLGLPLVLQAGFLLTKILTIPOSLSWTSNLFGLGPTVCLGNSQSISS 60
DB 163 NMENITSGFLGLPLVLQAGFLLTKILTIPOSLSWTSNLFGLGTTVCLGNSQSPSTN 222
QY 61 HSPTCCPPICGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
DB 223 HSPTSCPTCPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 282
QY 121 PKCTCTTAAQGTSMFPCSCCTKPTDRNCTCIPSSWAFKYLWENASVRFSLVLPV 180
DB 283 PCRTCTTAAQGTSMYPCSCCTKPSDGNCTCIPSSWAFKFLWENASVRFSLVLPV 342
RESULT 13
VMSA HPBV9
ID VMSA HPBV9 STANDARD; PRT; 400 AA.
AC P17101;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)

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DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adw / strain 991).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10410;
RN [1]
RP SEQUENCE FROM N.A.
RA Koehel H.G., Schueler A., Lottmann S., Thomsen R.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
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DR EMBL; X51970; CAA36230.1; -.
DR PIR; S10383; SAVLKS.
DR InterPro; IPR000349; Hepvir_surfac.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 174 MAJOR SURFACE ANTIGEN.
FT CHAIN 175 400
FT CARBOHYD 15 15 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 400 AA; 43695 MW; 76D98F74B8B17724 CRC64;
SQ SEQUENCE 400 AA; 43695 MW; 76D98F74B8B17724 CRC64;

Query Match 90.6%; Score 1161; DB 1; Length 400;
Best Local Similarity 90.7%; Pred. No. 9e-93;
Matches 206; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 NMENTASGLGLPVLVQAGFFLLTKILTIPOSLDSWMTSLNFLGGPTVCLGQNSQSQISS 60
DB 174 NMENTSGGLPGLPVLVQAGFFLLTKILTIPOSLDSWMTSLNFLGGSPVCLGQNSRPTSN 233
QY 61 HSPTCCPPICPGYRWMLRRFIIFLCILLCILFLLVLDYQGMPLVPCPLIPGTTTTSTG 120
DB 234 HSPTCCPPICPGYRWMLRRFIIFLCILLCILFLLVLDYQGMPLVPCPLIPGTTTTSTG 293
QY 121 PKCTCTTPAGTSMFPSCCCTKPTDNCCTCIPSSWAFAPKYLWASVRFSLVLLVPPF 180
DB 294 PKCTCTTPAGTSMFPSCCCTKPTDNCCTCIPSSWAFAPKYLWASVRFSLVLLVPPF 353
QY 181 VQWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPFMPLLPFIFFCLWYI 227
DB 354 VQWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPFMPLLPFIFFCLWYI 400

RESULT 14
VMSA_HPBVN STANDARD; PRT; 226 AA.
AC P30019;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus (subtype adr / strain NC-1).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31513;
RN [1]
RP SEQUENCE FROM N.A.
RA Qi Z.H., Yan J., Xiong W.J., Cai L.W.;
RL "Determination of the nucleotide sequence and studies on the
RT structure of hepatitis B virus (HBV) adr NC-1 surface antigen (HBsAg)
RT gene."
RL Sheng Wu Hua Hsueh Tsa Chih 4:201-209 (1988).
DR PIR; JC1002; SAVLNI.
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DR InterPro; IPR000349; Hepvir_surfac.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 226 AA; 25397 MW; 90FC24FA074B66AF CRC64;

Query Match 90.5%; Score 1159; DB 1; Length 226;
Best Local Similarity 89.8%; Pred. No. 7.8e-93;
Matches 203; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 2 MENIASGLGLPVLVQAGFFLLTKILTIPOSLDSWMTSLNFLGGPTVCLGQNSQSQISSH 61
DB 1 MENTASGLGLPVLVQAGFFLLTKILTIPOSLDSWMTSLNFLGGAPTCTGQNSQSPTSNH 60
QY 62 SPTCCPPICPGYRWMLRRFIIFLCILLCILFLLVLDYQGMPLVPCPLIPGTTTTSTGP 121
DB 61 SPTCCPPICPGYRWMLRRFIIFLCILLCILFLLVLDYQGMPLVPCPLIPGTTTTSTGP 120
QY 122 CKTCTTPAGTSMFPSCCCTKPTDNCCTCIPSSWAFAPKYLWASVRFSLVLLVPPFV 181
DB 121 CKTCTTPAGTSMFPSCCCTKPSDGNCTCIPSSWAFARFLWASVRFSLVLLVPPFV 180
QY 182 QWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPFMPLLPFIFFCLWYI 227
DB 181 QWFGVLSPTVWLSVIMWMMFWGSPSLYNILSPFMPLLPFIFFCLWYI 226

RESULT 15
VMSA_HPBVZ STANDARD; PRT; 389 AA.
ID VMSA_HPBVZ
AC P03139;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last annotation update)
DE Major surface antigen precursor.
GN S.
OS Hepatitis B virus (subtype adyw).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10419;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012115; PubMed=399329;
RA Pasek M., Goto T., Gilbert W., Zink B., Schaller H., Mackay P.,
RA Leadbetter G., Murray K.;
RT "Hepatitis B virus genes and their expression in E. coli.";
RL Nature 282:575-579 (1979).
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DR EMBL; J02202; AAA45487.1; ALT_INIT.
DR PIR; A93217; SAVLAJ.
DR InterPro; IPR000349; Hepvir_surfac.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT PROPEP 1 163 MAJOR SURFACE ANTIGEN.
FT CHAIN 164 389
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 389 AA; 42801 MW; 1069EF6B4679A669 CRC64;

Query Match 90.5%; Score 1159; DB 1; Length 389;
Best Local Similarity 89.4%; Pred. No. 1.3e-92;
Matches 203; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 NMENTASGLGLPVLVQAGFFLLTKILTIPOSLDSWMTSLNFLGGPTVCLGQNSQSQISS 60
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Db      163  N N E N I T S G F L G P L L V L Q A G F F L L T R L T I P Q S L D S W M T S L N F L G G T T V C L G N S Q S P I S N 222
QY      61   H S P T C C P P I C P G Y R W M C L R R F I F L C I L L C L I F L L V L L D Y Q G M L P V C P L I P G S T T T S T G 120
Db      223  H S P T S C P P T C P G Y R W M C L R R F I F L F I L L C L I F L L V L L D Y Q G M L P V C P L I P G S T T S T G 282
QY      121  P C K T C T T P A Q G T S M F P S C C C T K P T D R N C T C I P S S W A F A K Y L W E W A S V R F S W L S L L V P F 180
Db      283  S C R I C T T P A Q G I S M Y P S C C C T R P S D G N C T C I P I P S S W A F G K F L W E W A S A R F S W L S L L V P F 342
QY      181  V Q M F V G L S P T V M L S V I W M W M G P S L Y N I L S P F M P L L P I F F C L W V Y I 227
Db      343  V Q M F V G L S P I V M L S V I W M W M G P S L Y S I L S P F L P I L P I F F C L W A Y I 389

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Search completed: July 26, 2004, 11:27:38
 Job time : 16.528 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2004, 11:22:09 ; Search time 59.928 Seconds

(without alignments)
1195.145 Million cell updates/sec

Title: US-09-719-533A-3_COPY_174_400

Perfect score: 1281

Sequence: 1 NMENIASGLLGPLVLQAGF.....NILSPFPLPIFFCLWYI 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1256	98.0	281	12 Q9PX15	Q9px15 hepatitis b
2	1256	98.0	281	12 Q9QAC8	Q9qac8 hepatitis b
3	1256	98.0	281	12 Q9IC11	Q9ic11 hepatitis b
4	1256	98.0	400	12 Q9QSD0	Q9qsd0 hepatitis b
5	1256	98.0	400	12 Q9QAC9	Q9qac9 hepatitis b
6	1256	98.0	400	12 Q9PMW3	Q9pmw3 hepatitis b
7	1256	98.0	400	12 Q9TDO9	Q9tdo9 hepatitis b
8	1253	97.8	281	12 Q9QBF4	Q9qbf4 hepatitis b
9	1253	97.8	400	12 Q9QMI8	Q9qmi8 hepatitis b
10	1253	97.8	400	12 Q9QBF5	Q9qbf5 hepatitis b
11	1253	97.8	400	12 Q9QCH28	Q9qch28 hepatitis b
12	1253	97.8	400	12 Q9TDT0	Q9tdt0 hepatitis b
13	1252	97.7	281	12 Q9TDO9	Q9tdo9 hepatitis b
14	1252	97.7	281	12 Q9QAE6	Q9gae6 hepatitis b
15	1252	97.7	400	12 Q9QAE7	Q9gae7 hepatitis b
16	1252	97.7	400	12 Q67938	Q67938 hepatitis b

17	1250	97.6	226	12 Q9YIY6	Q9yiy6 hepatitis b
18	1248	97.4	281	12 Q7THP8	Q7thp8 hepatitis b
19	1248	97.4	400	12 Q9IF48	Q9if48 hepatitis b
20	1248	97.4	400	12 Q7THP9	Q7thp9 hepatitis b
21	1247	97.3	226	12 Q9QBF9	Q9qbf9 hepatitis b
22	1247	97.3	400	12 Q81135	Q81135 hepatitis b
23	1247	97.3	400	12 Q81117	Q81117 hepatitis b
24	1246	97.3	226	12 Q9QAF0	Q9qaf0 hepatitis b
25	1246	97.3	226	12 Q67934	Q67934 hepatitis b
26	1246	97.3	226	12 Q8JXE3	Q8jxe3 hepatitis b
27	1246	97.3	226	12 Q8QJ62	Q8qj62 hepatitis b
28	1246	97.3	281	12 Q9QAC2	Q9qac2 hepatitis b
29	1246	97.3	380	12 Q9QMN2	Q9qmn2 hepatitis b
30	1246	97.3	400	12 Q9QAC3	Q9qac3 hepatitis b
31	1245	97.2	226	12 Q8JXB6	Q8jxb6 hepatitis b
32	1245	97.2	445	12 Q9YKJ7	Q9ykj7 hepatitis b
33	1244	97.1	281	12 Q8QGV6	Q8qgv6 hepatitis b
34	1244	97.1	400	12 Q8QGV7	Q8qgv7 hepatitis b
35	1243	97.0	226	12 Q8JXC5	Q8jxc5 hepatitis b
36	1243	97.0	226	12 Q8QJ86	Q8qj86 hepatitis b
37	1243	97.0	281	12 Q9QBE0	Q9qbe0 hepatitis b
38	1243	97.0	400	12 Q9QBE1	Q9qbe1 hepatitis b
39	1242	97.0	226	12 Q72531	Q72531 hepatitis b
40	1242	97.0	226	12 Q8JXD5	Q8jxd5 hepatitis b
41	1242	97.0	226	12 Q8JXD3	Q8jxd3 hepatitis b
42	1242	97.0	226	12 Q8QJ82	Q8qj82 hepatitis b
43	1242	97.0	226	12 Q8QJ76	Q8qj76 hepatitis b
44	1242	97.0	226	12 Q7THP7	Q7thp7 hepatitis b
45	1242	97.0	281	12 Q9QAD2	Q9qad2 hepatitis b

ALIGNMENTS

RESULT 1

Q9PX15 ID Q9PX15 PRELIMINARY; PRT; 281 AA.
AC Q9PX15;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Middle S protein (Major surface antigen).
S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HBV/TK29902, HBV/95-14611, and HBV/92-16091;
RX MEDLINE=20109034; PubMed=10640544;
RA Hannoun C., Horal P., Lindh M.;
RT "Long-term mutation rates in the hepatitis B virus genome.";
RL J. Gen. Virol. 81:75-83(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HBV/TK29902, HBV/95-14611, and HBV/92-16091;
RA Hannoun C., Horal P., Lindh M.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF121246; AAF24709.1; -
DR EMBL; AF121243; AAF24688.1; -
DR EMBL; AF121245; AAF24702.1; -
DR PIR; JQ2059; JQ2059.
DR PIR; JQ2060; JQ2060.
DR PIR; JQ2062; JQ2062.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfac.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 281 AA; 31166 MW; 7C0F376ABE0443D4 CRC64;

Query Match 98.0%; Score 1256; DB 12; Length 281;
Best Local Similarity 98.2%; Pred. No. 1.9e-117;
Matches 223; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RA Huang W.J., Zhang H.Y., Wang Y.C., Wu X., Gu W.J., Ling J.X.,
RA Lan H.Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF479684; AAL86446.1; -;
DR PIR; JQ2059; JQ2059.
DR PIR; JQ2060; JQ2060.
DR PIR; JQ2062; JQ2062.
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR00349; Hepvir_surfac.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 400 AA; 43710 MW; C9C79C3B59B46D2C CRC64;

Query Match 98.0%; Score 1256; DB 12; Length 400;
Best Local Similarity 98.2%; Pred. No. 2.7e-117;
Matches 223; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMENIASGLGLPGLVLQAGFFLLTKLTIPQSLDSWNTSLNFLGGTPVCLGQNSQSQISS 60
Db 174 NMENIASGLGLPGLVLQAGFFLLTKLTIPQSLDSWNTSLNFLGGTPVCLGQNSQSQISS 233

QY 61 HSPTCCPPICPGYRWNCRLRRFIIFLCILLCLIFLLVLDYQGMPLVCPPLIPGSGTTSTG 120
Db 234 HSPTCCPPICPGYRWNCRLRRFIIFLCILLCLIFLLVLDYQGMPLVCPPLIPGSGTTSTG 293

QY 121 PKCTCTTTPAQTSMFPSCCCTKPTDNCCTCIPSSWAFKYLWENASVRFSLSLVVPF 180
Db 294 PKCTCTTTPAQTSMFPSCCCTKPTDNCCTCIPSSWAFKYLWENASVRFSLSLVVPF 353

QY 181 VQMFVGLSPTVWLSVIWMMFWGSPSLYNILSPFMPLLPIFFCLWVYI 227
Db 354 VQMFVGLSPTVWLSVIWMMFWGSPSLYNILSPFMPLLPIFFCLWVYI 400

RESULT 5
QOQAC9 PRELIMINARY; PRT; 400 AA.
AC QOQAC9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Large S protein (Major surface antigen).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HBV/4014;
RX MEDLINE=20109034; PubMed=10640544;
RA Hannoun C., Horal P., Lindh M.;
RT "Long-term mutation rates in the hepatitis B virus genome."
RL J. Gen. Virol. 81:75-83(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HBV/4014;
RA Hannoun C., Horal P., Lindh M.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF121249; AAF24728.1; -;
DR PIR; JQ2059; JQ2060.
DR PIR; JQ2062; JQ2062.
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR00349; Hepvir_surfac.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 400 AA; 43706 MW; 521F4D997BB3101B CRC64;

Query Match 98.0%; Score 1256; DB 12; Length 400;
Best Local Similarity 98.2%; Pred. No. 2.7e-117;
Matches 223; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMENIASGLGLPGLVLQAGFFLLTKLTIPQSLDSWNTSLNFLGGTPVCLGQNSQSQISS 60

Db 174 NMENIASGLGLPGLVLQAGFFLLTKLTIPQSLDSWNTSLNFLGGTPVCLGQNSQSQISS 233

QY 61 HSPTCCPPICPGYRWNCRLRRFIIFLCILLCLIFLLVLDYQGMPLVCPPLIPGSGTTSTG 120
Db 234 HSPTCCPPICPGYRWNCRLRRFIIFLCILLCLIFLLVLDYQGMPLVCPPLIPGSGTTSTG 293

QY 121 PKCTCTTTPAQTSMFPSCCCTKPTDNCCTCIPSSWAFKYLWENASVRFSLSLVVPF 180
Db 294 PKCTCTTTPAQTSMFPSCCCTKPTDNCCTCIPSSWAFKYLWENASVRFSLSLVVPF 353

QY 181 VQMFVGLSPTVWLSVIWMMFWGSPSLYNILSPFMPLLPIFFCLWVYI 227
Db 354 VQMFVGLSPTVWLSVIWMMFWGSPSLYNILSPFMPLLPIFFCLWVYI 400

RESULT 6
QOQAC9 PRELIMINARY; PRT; 400 AA.
AC QOQAC9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Large S protein (Major surface antigen).
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HBV/4014;
RX MEDLINE=20109034; PubMed=10640544;
RA Hannoun C., Horal P., Lindh M.;
RT "Long-term mutation rates in the hepatitis B virus genome."
RL J. Gen. Virol. 81:75-83(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HBV/4014;
RA Hannoun C., Horal P., Lindh M.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF121246; AAF24708.1; -;
DR PIR; JQ2059; JQ2060.
DR PIR; JQ2062; JQ2062.
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR00349; Hepvir_surfac.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 400 AA; 43750 MW; CE6F6A9093879343 CRC64;

Query Match 98.0%; Score 1256; DB 12; Length 400;
Best Local Similarity 98.2%; Pred. No. 2.7e-117;
Matches 223; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMENIASGLGLPGLVLQAGFFLLTKLTIPQSLDSWNTSLNFLGGTPVCLGQNSQSQISS 60
Db 174 NMENIASGLGLPGLVLQAGFFLLTKLTIPQSLDSWNTSLNFLGGTPVCLGQNSQSQISS 233

QY 61 HSPTCCPPICPGYRWNCRLRRFIIFLCILLCLIFLLVLDYQGMPLVCPPLIPGSGTTSTG 120
Db 234 HSPTCCPPICPGYRWNCRLRRFIIFLCILLCLIFLLVLDYQGMPLVCPPLIPGSGTTSTG 293

QY 121 PKCTCTTTPAQTSMFPSCCCTKPTDNCCTCIPSSWAFKYLWENASVRFSLSLVVPF 180
Db 294 PKCTCTTTPAQTSMFPSCCCTKPTDNCCTCIPSSWAFKYLWENASVRFSLSLVVPF 353

QY 181 VQMFVGLSPTVWLSVIWMMFWGSPSLYNILSPFMPLLPIFFCLWVYI 227
Db 354 VQMFVGLSPTVWLSVIWMMFWGSPSLYNILSPFMPLLPIFFCLWVYI 400

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RESULT 7
Q7TDQ9 ID Q7TDQ9 PRELIMINARY; PRT; 400 AA.
AC Q7TDQ9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Presl/pres2 surface protein.
OS Hepatitis B virus.
OC Viruses; Retrod viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IIB;
RA Liu C.-J., Chen P.-J., Lai M.-Y., Kao J.-H., Chen D.-S.;
RT "A prospective study characterizing full-length hepatitis B virus
RT genomes during acute exacerbation."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY167097; AAO41318.1; -.
SQ SEQUENCE 400 AA; 43731 MW; 221E3860873CDB6E CRC64;

Query Match 98.0%; Score 1256; DB 12; Length 400;
Best Local Similarity 98.2%; Pred. No. 2.7e-117;
Matches 223; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMENIASGLLGLLVLQAGFFLLTKILTIPOSLDSWMTSLNPLGGPTVCLGNSQSQISS 60
Db 174 NMENIASGLLGLLVLQAGFFLLTKILTIPOSLDSWMTSLNPLGGPTVCLGNSQSQISS 233

QY 61 HSPTCCPPICPGYRWMLRRFIIFLCILLCILFLLVLDYQGMPLVPCPLIPGSGTTSTG 120
Db 234 HSPTCCPPICPGYRWMLRRFIIFLCILLCILFLLVLDYQGMPLVPCPLIPGSGTTSTG 293

QY 121 PKCTCTTAAQGTSMFPSCCCTKPTDRNCTCIPSSWAFAYLWESVRSWLSLVPF 180
Db 294 PKCTCTTAAQGTSMFPSCCCTKPTDRNCTCIPSSWAFAYLWESVRSWLSLVPF 353

QY 181 VQWVGLSPTVWLSVIMWFWGSPSLYNILSPFMPLPIFFCLWYI 227
Db 354 VQWVGLSPTVWLSVIMWFWGSPSLYNILSPFMPLPIFFCLWYI 400

RESULT 8
Q9QBF4 ID Q9QBF4 PRELIMINARY; PRT; 281 AA.
AC Q9QBF4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE M protein (Major surface antigen) (Middle S protein).
OS Hepatitis B virus.
OC Viruses; Retrod viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Yamagata-1;
RA Koseki T., Hongo S., Muraki Y., Sugawara K., Matsuzaki Y.,
RA Nakamura K.;
RT "Sequence analysis of the entire genome of hepatitis B virus from a
RT patient with fulminant hepatitis."
RL Yamagata Med. J. 17:27-40(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FMU06;
RA Lin X., Zheng D.L., Xu X.;
RT "Genotype distribution of HBV from hepatocellular carcinoma tissues."
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010289; BAA88277.1; -.
DR EMBL; AY206377; AAP06552.1; -.
DR PIR; JQ2059; JQ2059.
DR PIR; JQ2060; JQ2060.
DR PIR; JQ2062; JQ2062.
DR GO; GO:0016032; P: viral life cycle; IEA.

Query Match 97.8%; Score 1253; DB 12; Length 400;
Best Local Similarity 97.8%; Pred. No. 5.4e-117;
Matches 222; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMENIASGLLGLLVLQAGFFLLTKILTIPOSLDSWMTSLNPLGGPTVCLGNSQSQISS 60
Db 174 NMENIASGLLGLLVLQAGFFLLTKILTIPOSLDSWMTSLNPLGGPTVCLGNSQSQISS 233

QY 61 HSPTCCPPICPGYRWMLRRFIIFLCILLCILFLLVLDYQGMPLVPCPLIPGSGTTSTG 120
Db 234 HSPTCCPPICPGYRWMLRRFIIFLCILLCILFLLVLDYQGMPLVPCPLIPGSGTTSTG 293

QY 121 PKCTCTTAAQGTSMFPSCCCTKPTDRNCTCIPSSWAFAYLWESVRSWLSLVPF 180
Db 294 PKCTCTTAAQGTSMFPSCCCTKPTDRNCTCIPSSWAFAYLWESVRSWLSLVPF 353

QY 181 VQWVGLSPTVWLSVIMWFWGSPSLYNILSPFMPLPIFFCLWYI 227
Db 354 VQWVGLSPTVWLSVIMWFWGSPSLYNILSPFMPLPIFFCLWYI 400

RESULT 9
Q9QM18 ID Q9QM18 PRELIMINARY; PRT; 400 AA.
AC Q9QM18;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Presl/pres2/S envelope (Major surface antigen).
GN PRES1/PRES2/S.
OS Hepatitis B virus.
OC Viruses; Retrod viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=genotype B;
RA Okamoto H.;
RA Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=genotype B;
RA Sastrosuewignjo R.I., Okamoto H., Mayumi M., Rustam M., Warsa U.C.,
RA Sujudi X.;
RT "The complete nucleotide sequence of an HBV DNA clone of subtype adw
RT (pAD744) from Sumatra, Indonesia."
RL ICMR Ann. 6:99-106(1986).
DR EMBL; AB033555; BAA85344.1; -.
DR PIR; JQ2059; JQ2059.
DR PIR; JQ2060; JQ2060.
DR PIR; JQ2062; JQ2062.
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfa.
DR Pfam; PF00695; vmsa; 1.
KW Antigen.
SQ SEQUENCE 400 AA; 43804 MW; 26C03CE0E9A3CD1A CRC64;

Query Match 97.8%; Score 1253; DB 12; Length 400;
Best Local Similarity 97.8%; Pred. No. 5.4e-117;
Matches 222; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMENIASGLLGLLVLQAGFFLLTKILTIPOSLDSWMTSLNPLGGPTVCLGNSQSQISS 60
Db 174 NMENIASGLLGLLVLQAGFFLLTKILTIPOSLDSWMTSLNPLGGPTVCLGNSQSQISS 233

QY 61 HSPTCCPPICPGYRWMLRRFIIFLCILLCILFLLVLDYQGMPLVPCPLIPGSGTTSTG 120
Db 234 HSPTCCPPICPGYRWMLRRFIIFLCILLCILFLLVLDYQGMPLVPCPLIPGSGTTSTG 293
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Q67939
ID Q67939 PRELIMINARY; PRT; 281 AA.
AC Q67939;
DT 01-NOV-1996 (TremBrel. 01, Created)
DT 01-NOV-1996 (TremBrel. 01, Last sequence update)
DT 01-OCT-2003 (TremBrel. 25, Last annotation update)
DE Pre-S2 protein (Major surface antigen).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97025699; PubMed=8871878;
RA Alexopoulos A., Kariyannis P., Hadziyannis S.J.;
RT "Whole genome analysis of hepatitis B virus from 4 cases with
RT fulminant hepatitis.";
RL J. Viral Hepat. 3:173-181(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Karayannis P.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97851; CAA66446.1; -.
DR PIR; JQ2059; JQ2059.
DR PIR; JQ2060; JQ2060.
DR PIR; JQ2062; JQ2062.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfac.
DR Pfam; PF00695; vNSA; 1.
KW Antigen.
SQ SEQUENCE 281 AA; 31243 MW; 67710167D17A06D4 CRC64;

Query Match 97.7%; Score 1252; DB 12; Length 281;
Best Local Similarity 97.8%; Pred. No. 4.8e-117;
Matches 222; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NMENIASGLLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 60
Db 55 NMENITSLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 114
QY 61 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
Db 115 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 174
QY 121 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 180
Db 175 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 234
QY 181 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 227
Db 235 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 281

RESULT 14
Q67939 PRELIMINARY; PRT; 281 AA.
AC Q67939;
DT 01-MAY-2000 (TremBrel. 13, Created)
DT 01-MAY-2000 (TremBrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBrel. 25, Last annotation update)
DE Middle S protein (Major surface antigen).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20109034; PubMed=10640544;
RA Hannoun C., Horal P., Lindh M.;
RT "Long-term mutation rates in the hepatitis B virus genome.";
RL J. Gen. Virol. 81:75-83(2000).
RN [2]
RP SEQUENCE FROM N.A.

QY 1 NMENIASGLLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 60
Db 55 NMENITSLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 114
QY 61 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
Db 115 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 174
QY 121 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 180
Db 175 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 234
QY 181 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 227
Db 235 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 281

RESULT 15
Q67939 PRELIMINARY; PRT; 400 AA.
AC Q67939;
DT 01-MAY-2000 (TremBrel. 13, Created)
DT 01-MAY-2000 (TremBrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBrel. 25, Last annotation update)
DE Large S protein (Major surface antigen).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20109034; PubMed=10640544;
RA Hannoun C., Horal P., Lindh M.;
RT "Long-term mutation rates in the hepatitis B virus genome.";
RL J. Gen. Virol. 81:75-83(2000).
RN [2]
RP SEQUENCE FROM N.A.

QY 1 NMENIASGLLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 60
Db 55 NMENITSLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 114
QY 61 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
Db 115 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 174
QY 121 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 180
Db 175 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 234
QY 181 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 227
Db 235 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 281

Query Match 97.7%; Score 1252; DB 12; Length 281;
Best Local Similarity 97.8%; Pred. No. 4.8e-117;
Matches 222; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NMENIASGLLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 60
Db 55 NMENITSLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 114
QY 61 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
Db 115 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 174
QY 121 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 180
Db 175 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 234
QY 181 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 227
Db 235 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 281

Query Match 97.7%; Score 1252; DB 12; Length 281;
Best Local Similarity 97.8%; Pred. No. 4.8e-117;
Matches 222; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMENIASGLLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 60
Db 55 NMENITSLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 114
QY 61 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
Db 115 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 174
QY 121 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 180
Db 175 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 234
QY 181 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 227
Db 235 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 281

Query Match 97.7%; Score 1252; DB 12; Length 400;
Best Local Similarity 97.8%; Pred. No. 6.8e-117;
Matches 222; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMENIASGLLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 60
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Q67939
ID Q67939 PRELIMINARY; PRT; 281 AA.
AC Q67939;
DT 01-NOV-1996 (TremBrel. 01, Created)
DT 01-NOV-1996 (TremBrel. 01, Last sequence update)
DT 01-OCT-2003 (TremBrel. 25, Last annotation update)
DE Pre-S2 protein (Major surface antigen).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97025699; PubMed=8871878;
RA Alexopoulos A., Kariyannis P., Hadziyannis S.J.;
RT "Whole genome analysis of hepatitis B virus from 4 cases with
RT fulminant hepatitis.";
RL J. Viral Hepat. 3:173-181(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Karayannis P.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97851; CAA66446.1; -.
DR PIR; JQ2059; JQ2059.
DR PIR; JQ2060; JQ2060.
DR PIR; JQ2062; JQ2062.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfac.
DR Pfam; PF00695; vNSA; 1.
KW Antigen.
SQ SEQUENCE 281 AA; 31243 MW; 67710167D17A06D4 CRC64;

Query Match 97.7%; Score 1252; DB 12; Length 281;
Best Local Similarity 97.8%; Pred. No. 4.8e-117;
Matches 222; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NMENIASGLLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 60
Db 55 NMENITSLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 114
QY 61 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
Db 115 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 174
QY 121 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 180
Db 175 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 234
QY 181 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 227
Db 235 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 281

RESULT 14
Q67939 PRELIMINARY; PRT; 281 AA.
AC Q67939;
DT 01-MAY-2000 (TremBrel. 13, Created)
DT 01-MAY-2000 (TremBrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBrel. 25, Last annotation update)
DE Middle S protein (Major surface antigen).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20109034; PubMed=10640544;
RA Hannoun C., Horal P., Lindh M.;
RT "Long-term mutation rates in the hepatitis B virus genome.";
RL J. Gen. Virol. 81:75-83(2000).
RN [2]
RP SEQUENCE FROM N.A.

QY 1 NMENIASGLLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 60
Db 55 NMENITSLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 114
QY 61 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
Db 115 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 174
QY 121 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 180
Db 175 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 234
QY 181 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 227
Db 235 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 281

RESULT 15
Q67939 PRELIMINARY; PRT; 281 AA.
AC Q67939;
DT 01-MAY-2000 (TremBrel. 13, Created)
DT 01-MAY-2000 (TremBrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBrel. 25, Last annotation update)
DE Large S protein (Major surface antigen).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20109034; PubMed=10640544;
RA Hannoun C., Horal P., Lindh M.;
RT "Long-term mutation rates in the hepatitis B virus genome.";
RL J. Gen. Virol. 81:75-83(2000).
RN [2]
RP SEQUENCE FROM N.A.

QY 1 NMENIASGLLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 60
Db 55 NMENITSLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 114
QY 61 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
Db 115 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 174
QY 121 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 180
Db 175 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 234
QY 181 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 227
Db 235 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 281

Query Match 97.7%; Score 1252; DB 12; Length 281;
Best Local Similarity 97.8%; Pred. No. 4.8e-117;
Matches 222; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NMENIASGLLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 60
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Db 115 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 174
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Db 175 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 234
QY 181 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 227
Db 235 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 281

Query Match 97.7%; Score 1252; DB 12; Length 281;
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QY 61 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 120
Db 115 HSPTCCPPICPGYRWMLRRRIIFLCILLCLIFLLVLDYQGMPLVCPILPGSTTTSTG 174
QY 121 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 180
Db 175 PKCTTTTAAQGTSMFPSCCTKPTDRNCTCIPSSWAFAYLWEMASVRFSLSLVVPF 234
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Db 235 VQWFGVLSPTVWLSVINWMMFWGSLNLSLSPFMPPLLPFFCLWYI 281

Query Match 97.7%; Score 1252; DB 12; Length 400;
Best Local Similarity 97.8%; Pred. No. 6.8e-117;
Matches 222; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMENIASGLLGLLVQAGFLLTKILTIPOSLSWNTSLNPLGQPTVCLGQNSQSQISS 60
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Qy	121	PKTCTTQAQCTSMFPSCCCTKPTDRNCTCIPISWAFKYLWENASVRFSLSLVPP	180
Db	294	PKTCTTQAQCTSMFPSCCCTKPTDRNCTCIPISWAFKYLWENASVRFSLSLVPP	353
Qy	181	VQWFGLSPTVWLSVINWMMFWGPSLXNLSPPFLLPIPFCLWYI	227
Db	354	VQWFGLSPTVWLSVINWMMFWGPSLXNLSPPFLLPIPFCLWYI	400

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